

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2002, 16:49:54 ; Search time 2229.59 Seconds  
(without alignments)  
16519.048 Million cell updates/sec

Title: US-09-786-835-1

Perfect score: 1760

Sequence: 1 ctcgagatgtgtagatagaag.....gtcatcatcatcatcactcca 1760

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl1.\*  
1: gb\_ba.\*  
2: gb\_hlg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_inv.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C	1	76.4	4.3	3203	8	MZETRNBS1	M25397 Zea mays tr
C	2	76.4	4.3	3203	8	ZMB51RET	X16080 Maize trans
C	3	75.6	4.3	488	11	G71285	G71285 VF044831FM
C	4	62.2	3.5	7218	6	I66494	I66494 Sequence 14
C	5	61	3.5	4648	8	AF326577	AF326577 Zea mays
C	6	53.4	3.0	78101	8	AF031569	AF031569 Zea mays
C	7	53.4	3.0	346296	8	AF090447	AF090447 Zea mays
C	8	53.2	3.0	147198	8	AF466203	AF466203 Zea mays
C	9	51.2	2.9	172805	2	AC066608	AC066608 Homo sapi
C	10	50	2.8	70282	2	AC091141	AC091141 Homo sapi
C	11	49.8	2.8	78167	9	AC092028	AC092028 Homo sapi
C	12	48.8	2.8	5026	6	AX251272	AX251272 Sequence
C	13	48.4	2.8	7503	6	AX346677	AX346677 Sequence
C	14	47.8	2.7	189790	2	AC107420	AC107420 Homo sapi
C	15	47.2	2.7	5416	6	AX346698	AX346698 Sequence
C	16	47	2.7	7753	8	ZMAYSP6	Z11879 Z.mays P ge
C	17	47	2.7	173655	2	OSJN00181	AL662993 Oryza sat
C	18	46.8	2.7	349980	6	AX344566	AX344566 Sequence
C	19	46.8	2.7	349980	6	AX344567	AX344567 Sequence
C	20	46.4	2.6	208396	9	AC003101	AC003101 Homo sapi
C	21	46.2	2.6	28021	3	CELY37E11B	AF125451 Caenorhab
C	22	46.2	2.6	155880	2	AC006739	AC006739 Caenorhab
C	23	46	2.6	349980	6	AX344563	AX344563 Sequence
C	24	46	2.6	349980	6	AX344564	AX344564 Sequence
C	25	45.8	2.6	676	8	PTR286131	AJ286131 Populus t
C	26	45.8	2.6	47577	3	AF396436	AF396436 Tetrahyme
C	27	45.8	2.6	173943	2	AC013293	AC013293 Homo sapi
C	28	45.8	2.6	213007	2	AC105762	AC105762 Homo sapi
C	29	45.6	2.6	99003	2	AL390756	AL390756 Homo sapi
C	30	45.6	2.6	191580	2	AC092945	AC092945 Homo sapi
C	31	45.6	2.6	205141	2	AC018679	AC018679 Homo sapi
C	32	45.4	2.6	6412	6	AX251842	AX251842 Sequence
C	33	45.4	2.6	6412	6	AX344228	AX344228 Sequence
C	34	45.4	2.6	6412	6	AX344644	AX344644 Sequence
C	35	45.4	2.6	6412	6	AX348967	AX348967 Sequence
C	36	45.4	2.6	178087	9	AC005089	AC005089 Homo sapi
C	37	45.2	2.6	1200	8	MISCA	V00705 Yeast mitoc
C	38	45.2	2.6	3542	8	YSCMTCG16	L36900 Saccharomyc
C	39	45.2	2.6	14924	6	AX281279	AX281279 Sequence
C	40	45.2	2.6	14924	6	AX345126	AX345126 Sequence
C	41	45.2	2.6	85779	8	SCED11856	AJ011856 Saccharom
C	42	45	2.6	170991	2	AL645585	AL645585 Homo sapi
C	43	45	2.6	129730	2	AC083940	AC083940 Homo sapi
C	44	44.8	2.5	127197	6	AX196294	AX196294 Sequence
C	45	44.8	2.5	146957	2	AC078802	AC078802 Homo sapi

## ALIGNMENTS

RESULT 1  
MZETRNBS1/c 3203 bp DNA linear PLN 11-MAY-1995  
LOCUS MZETRNBS1 Zea mays transposon Bsl.  
DEFINITION M25397  
ACCESSION M25397.1 GI:168648  
VERSION  
KEYWORDS insertion sequence; transposon.  
SOURCE Zea mays (clone: PK18) 4-week-old seedlings aerial part DNA; and  
Ze mays (clone: pui) 4-week-old seedling aerial part DNA.  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 3203)  
AUTHORS Jin,Y.K. and Bennetzen,J.L.  
TITLE Structure and coding properties of Bsl, a maize retrovirus-like  
transposon  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86 (16), 6235-6239 (1989)  
MEDLINE 89345638  
COMMENT Draft entry and computer-readable sequence for [1] kindly provided  
by J.L.Bennetzen, 07-JUN-1989.  
FEATURES Location/Qualifiers  
source 1..3203

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2608 .

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IN							

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	st Local Similarity	69.3%;	Pred. No. 4.9e-09;		
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				Gaps	0;
1	ctcgaagatgttgatctgaaaggaatttcgagcaaccgaggtctccaaagcagccaaag	60			
478	cttcacagtcctggaatgcacctccgaattggcgcactgttcgcactccgcactccgcacacg	419			
61	cgcacatctgcgcagctagatgtgcgtctgattctgcgaagaagactcgaattgttcgcgat	120			
418	cgccttctctggcgcagcagcggcgctcactgattctgcgaagaagatcttcaactgtttccctcat	359			
121	cgcgaagcttcagaatttggtccatgaccc	150			
358	cgcgcagctcagagggtggcctccatgagacgc	329			

RESULT	2				
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LOCUS	ZMB51RET	3203 bp	DNA	linear	PLN 12-SEP-1992
DEFINITION	Maize transposable element Bst1.				
ACCESSION	X16080				
VERSION	X16080.1	GI:22198			
KEYWORDS	long terminal repeat; retrotransposon; reverse transcriptase; transposable element.				
SOURCE	Zea mays.				
ORGANISM	Zea mays.				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 3203)				
AUTHORS	Johns,M.A., Babcock,M.S., Fuerstenberg,S.M., Fuerstenberg,S.I., Freeling,M., and Simpson,R.B.				
TITLE	An unusually compact retrotransposon in maize				
JOURNAL	Plant Mol. Biol. 12, 633-642 (1989)				
FEATURES	Location/Qualifiers				

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275..280
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GTHTHTALTPRALHKKPLVAAHAKSTGHNHNGACEOTGROGROAROCRLVHVH
RLHETGTLALRHOGRORRHOVHOYORLCPGAEIDRGRLPMPVAVHDDREFRHLIO
HHTDPGGSGGSGITPPEVBMLSAAGYNAAAPAEVYVRYKTLGFLVMPRTYCIAG
IDGDEYABEGADHAAVRYRFRYIDCGVEYEGGTVCAEBSSEWTEIKCYFRILKRAHVEY
VQAVAGIDVATDPQVAFATVONLAVHVEFTRHFDPAVEKEFERHTRHVDAAVEY
KMLTKGEAPSVQGVYMTVAHNLVQALEMDRASDAVYALEMONNGPFDVFTY
TLVKNQGOAEEESTLLVPGDIIYGVALGDIISMDRLBEDPLKIDQSLATGNCNIC
SYAGMIVERTVMYPIODMYAPRIDKLVLVLLIGGIPLAMEYTVSYMSISATRYLAOC
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	promoter	/note="pot. TATA box"	3176..3181	
	misc_feature	/note="pot. polyadenylation site"	870 g 782 t	
BASE COUNT	738 a	813 c		
ORIGIN				
Query Match	4.3%	Score 76.4:	DB 8:	
Best Local Similarity	69.3%	Pred. No.	4.9e-09;	
Matches 104:	Conservative	0:	Mismatches 46:	Indels 0:
				Gaps 0:
Oy	1 ctccagatgttgcataagaagaaattcgagcaacgaggctctccaagcagcgaacy	60		
Dh	478 CTCGAGTCGTGGATCGACCTCGAATGTGGTGCTCCTGCATCCGCACTGCCGACCG	419		



SOURCE	Zea mays.
ORGANISM	Zea mays.
REFERENCE AUTHORS TITLE	Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea. 1 (bases 1 to 4648) Sellingner,D.A. and Chandler,V.L. B-Bollivia, an Allele of the Maize b1 Gene with Variable Expression, Contains a High Copy Retrotransposon-Related Sequence Immediately Upstream Plant Physiol. 125 (3), 1363-1379 (2001)
JOURNAL PUBMED	11244116
AUTHORS	2 (bases 1 to 4648) Sellingner,D.A. and Chandler,V.L.
TITLE	Direct Submission
JOURNAL	Submitted (06-DEC-2000) Department of Plant Sciences, University of Arizona, 303 Forbes Bldg. 36, Tucson, AZ 85721, USA
FEATURES	Location/Qualifiers
SOURCE	1..4648
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PROMOTER	
TATA_SIGNAL	
MRNA	
CDS	
BASE COUNT	988 A 1153 C 1284 G 1223 T
ORIGIN	
Query Match	3.5% Score 61; DB 8; Length 4648;
Best Local Similarity	66.3%; Pred. No. 6e-05;
Matches 124; Conservative	0; Mismatches 50; Indels 13; Gaps 2;
OY 846	tagtgctcaaaatggccaaaagtgttaaaaggatacctaattgttgcataaccct 905
DB 4461	TAGCAGCTTAAATTACCTAAGAGGTTTAAACAACATCAGCTATTATAGTTACTTCT 4520
OY 906	taaataagaattaatgttagat---ggccaacactgataaa-----ccagtt 952

Db	4521	AAATTAAGTATTAGTGTGTACTACTAAGCTAAACCAACGCTAACACACTATTATAGCCAACT	4580
Qy	953	aaccagttagctctaaatglttagaacatgacctaaacaacatattatgagctactcgc	1012
Db	4581	AACATTAAGCTTTAGAGSTTTGAATAGAGTCTGAACCACTACTGTAAAGGCATTACG	4640
Qy	1013	cgatcc	1019
Db	4641	AGGTGCC	4647
RESULT 6			
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LOCUS	AF031569		
DEFINITION	Zea mays 22-kDa alpha zein gene cluster, complete sequence.		
ACCESSION	AF031569		
VERSION	AF031569.1	GI:2832242	
KEYWORDS			
SOURCE			
ORGANISM	Zea mays.		
	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC		
	clade; Panicoidae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 78101)		
AUTHORS	Llaca,V. and Messing,J.		
TITLE	Structure and organization of the 22-kDa alpha zein gene cluster in		
	Zea mays		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 78101)		
AUTHORS	Llaca,V. and Messing,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-Oct-1997) Waksman Institute, Rutgers, The State		
	University of New Jersey, P.O. Box 759, Piscataway, NJ 08855-0759,		
	USA		
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SSPLPAATLIQOOLLALQOOLIVPALTIQVLANPAILQOOLLPTNQLPNSASATLQOR
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23325. .24125
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25530. .68272
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41499. .42213
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41990. .78101
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		GRPPYA"
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	SSPLVGNAPTYLOOQLOOIVPALNQLAVANPAVYLOQILPENQILVSAGYLOO	
	QOLNPLAVNPPLYATFLQOQOQLPYQSFSLMNPVLAHQPIYOGALF"	
	58815.. .59610	
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	/note="22-kDa alpha zein 9"	
	/pseudo	
misc_feature	order(complement(67340..68552),68037..68563)	
	/note="similar to zea mays globulin-1 promoter"	
misc_feature	71597..72372	
	/note="similar to zea mays zrp2 promoter"	
gene	75093..75893	
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ORIGIN		
Query Match	3.0%: Score 53.4; DB 8; Length 78101;	
Best Local Similarity	53.9%: Pred. No. 0.0092;	
Matches 131; Conservative	0; Mismatches 111; Indels 1; Gaps 1;	
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Db	57789 ACTTATTTAGCTGATTAACAAATTAATTTTAAAGTTTGAACATGGCTTATCTCATGCT	57848
QY	998 tat 1000	
Db	57849 TCT 57851	
RESULT	7	
AF090447	346296 bp	DNA linear PLN 24-APR-2001
LOCUS		
DEFINITION	zea mays 22 kDa alpha zein gene cluster, complete sequence.	
ACCESSION	AF090447	AF105716
VERSION	AF090447.2	GI:13606087
KEYWORDS		

SOURCE	Zea mays.
ORGANISM	Zea mays. Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE AUTHORS TITLE	1 (bases 1 to 346296) Song, R., Liaca, V., Linton, E. and Messing, J. Genomic imprinting as a Rescue for a Compact Gene Cluster of Zea mays L.
JOURNAL REFERENCE AUTHORS TITLE	2 (bases 80292 to 116863) Song, R., Liaca, V. and Messing, J. Direct Submission Submitted (04-SEP-1998) Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
JOURNAL REFERENCE AUTHORS TITLE	3 (bases 1 to 65155) Liaca, V., Lou, A., Young, S. and Messing, J. Direct Submission Submitted (10-NOV-1998) Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
JOURNAL REFERENCE AUTHORS TITLE	4 (bases 1 to 346296) Song, R., Liaca, V. and Messing, J. Direct Submission Submitted (12-APR-2001) Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
JOURNAL REFERENCE AUTHORS TITLE	5 (bases 1 to 346296) Sequence update by submitter Song, R., Liaca, V. and Messing, J. Direct Submission Submitted (24-APR-2001) Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
REMARK COMMENT	Amino acid sequence updated by submitter On Apr 12, 2001 this sequence version replaced gi:4416300 gi:4140643.
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[illegible]

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D	204008	TAAAGGGCTCTATCTTAACCAATAATATTAGACGTAAATACAGTGAAGATTAGAAC 204067
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D	204187	TCT 204189

RESULT	8	
LOCUS	AF466203	
DEFINITION	147198 bp DNA linear PLN 07-FEB-2002	
ACCESSION	AF466203	
VERSION	AF466203.1	
KEYWORDS	GI:18568234	
SOURCE	Zea mays.	
ORGANISM	Zea mays.	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC	
AUTHORS	Glade, Panicoideae; Andropogoneae; Zea.	
JOURNAL	1 (bases 1 to 147198)	
REFERENCE	Ramakrishna, W., Sam Miguel, P., Emberton, J. and Bennetzen, J.	
REFERENCE	Submitted (07-JUN-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA	
REFERENCE	2 (bases 1 to 147198)	
REFERENCE	Liaca, V., Linton, E.W., Young, S., Kovchok, S. and Messing, J.	
REFERENCE	Submitted (07-JUN-2002) Rutgers, The State University of New Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA	
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Query Match	Best Local Similarity	Score	DB	Length
Matches 61; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	3.0%; 82.4%;	53.2;	DB 8;	147198;
Oy	856	aattagccaagaagtctgaatgatactaatctgttagctatacccttaataaagta	915	
Db	24141	AATTAGCTAAGAGGTTTGAACCCATCATTAATTGTTAGTTATACCCCTTAATAACTA	24200	
Oy	916	ttaactgttagatc	929	
Db	24201	CTAAGTTGTTAGCTG	24214	

RESULT

9



AC066608/c	LOCUS	172805 bp	DNA	linear	PRI 11-FEB-2001
AC066608	DEFINITION	Homo sapiens chromosome 3 clone RP11-785A7 map 3p, complete sequence.			
AC066608	ACCESSION				
AC066608.5	VERSION	GI:12745084			
AC066608	KEYWORDS				
SOURCE	ORGANISM	human.			
		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	AUTHORS	1 (bases 1 to 172805) Xiong,H., Zhou,Y., Dong,H., Lin,W., Chen,B., Zhang,C., Zhang,Y., Cai,Z., Ying,H.F., Wang,H., Gu,W., Zhu,G., Tu,Y., Zhang,X., Jia,J., Shen,H., Zhang,D., Wu,C., Lu,G., Zhong,M., Jiang,H., Ren,S., Fu,G., Chen,Z. and Huang,M.			
TITLE	JOURNAL	Chromosome 3p genomic sequence			
REFERENCE	AUTHORS	Unpublished 2 (bases 1 to 172805) Zhang,X., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J. and Yang,H.			
TITLE	JOURNAL	Direct Submission			
REFERENCE	AUTHORS	Submitted (25-APR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China 3 (bases 1 to 172805) Dong,Y., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Bao,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,C., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.			
TITLE	JOURNAL	Direct Submission			
COMMENT		Submitted (11-FEB-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China On Feb 11, 2001 this sequence version replaced gi:8101281.			
		-----Genome Center			
		Center:Beijing Center			
		Center code:Beijing			
		website:http://hgsc.igtp.ac.cn			
		http://www.genomics.org.cn			
		Contact:hgsc@igtp.ac.cn			
		-----Project Information			
		Center project name:18 project			
		Center clone name: RP11-785A7			
		----- Summary Statistics			
		Sequencing vector: pUC18: 100% of reads			
		Chemistry: Dye-terminator: ET 55% of reads			
		Chemistry: Dye-terminator Big Dye: 45% of reads			
		Assembly program: Phrap; version 0.990329			
		Consensus quality: 176043 bases at least Q40			
		Consensus quality: 176221 bases at least Q30			
		Consensus quality: 176261 bases at least Q20			
		Insert size: 172805; sum-of-contigs			
		Quality coverage: 8.12x in Q20 bases;sum-of-contigs			
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FEATURES	SOURCE				

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ORIGIN				
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Best Local Similarity	56.5%; Pred. No. 0.039; Indels 0; Gaps 0;			
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OY	816 attctgttcctaactcctcaaacctaagtgcagtgtgccaataataggccaaaggltaga 875                                                             Db 140448 TATATAATATATGTATTATATATATATATATATTTTTTATATAATATATAAATATATATATT 140389			
Oy	876 atggatacaacctaatgtgtaagcatcacctttaaataagtattaatgtt 923                                                                                  Db 140388 ATAATAAAATATATGTATATATATATATATATATTAATAATAATATATATATAT 140341			
RESULT 10				
AC091141				
LOCUS	AC091141 70282 bp DNA linear HTG 01-APR-2001			
DEFINITION	Homo sapiens chromosome 11 clone RP11-727K3 map 11, LOW-PASS SEQUENCE SAMPLING.			
ACCESSION	AC091141			
VERSION	AC091141.1 GI:13493106			
KEYWORDS	HTG; HTGS_PNASO.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 70282) Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 11, clone RP11-727K3 Unpublished 2 (bases 1 to 70282)			
AUTHORS	Biren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barne,R., Bastien,V., Boguslavsky,I., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collimore,A., Cooke,P., Debellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Glnde,S., Guyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heeford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRoque,K., Lamazeas,R., Landers,T., Lehoczkyl,U., Levine,R., Liu,G., MacLean,C., MacDonald,P., Marquis,N., Matthews,C., McCarthy,M., McManis,P., McKernan,K., MCPheeters,R., Meltrim,J., Menues,L., Mihova,T., Mianga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Nohman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retler,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Roselli,M., Roy,A., Santos,R., Schauer,S., Schnuppach,R., Seaman,S., Severi,P., Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamsz,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,U., Zemdek,L., Zimmer.A. and Zody.M.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA			
COMMENT	All repeats were identified using RepeatMasker: SmtL, A.F.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a> ----- Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WMR Web site: <a href="http://www-seq.wi.mit.edu">http://www-seq.wi.mit.edu</a> Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: LI2684 Center clone name: 727_K_3			

-----  
\* NOTE: This record contains 84 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
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\* 813 1577: contig of 765 bp in length  
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[illegible]











GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2002, 16:54:10 ; Search time 219.43 Seconds  
(without alignments)  
13770.995 Million cell updates/sec

Title: US-09-786-835-1

Perfect score: 1760  
Sequence: 1 ctccagatgttgatagaag.....ggtccatcatcatcactcca 1760

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1760	100.0	1760	21	AAZ52234
2	1760	100.0	3416	21	AAZ52247
3	1710	97.2	1710	21	AAZ52244
4	1550	88.1	1550	21	AAZ52243
5	1497	85.1	1497	21	AAZ52242
6	1354	76.9	1354	21	AAZ52241
7	1348	76.6	1348	21	AAZ52235
8	1096	62.3	1096	21	AAZ52236
9	746	42.4	746	21	AAZ52237

10	554	31.5	554	21	AAZ52238	Maize glycine-rich
11	406	23.1	406	21	AAZ52239	Maize glycine-rich
12	190	10.8	190	21	AAZ52240	Maize glycine-rich
13	48.8	2.8	5026	22	AAZ46518	Tumour suppressor
14	48.4	2.8	7503	22	ABL33775	Human immune system
15	47.2	2.7	5416	24	ABL33796	Human immune system
16	45.4	2.6	6412	24	AAZ56145	Human immune system
17	45.2	2.6	14924	22	AAZ61370	Human immune system
18	44.8	2.5	127197	22	AAZ61370	Human immune system
19	44.4	2.5	5452	24	ABL33149	Human immune system
20	44.2	2.5	17421	22	AAZ545349	Chemically induced
21	43.8	2.5	18154	24	ABL32254	Human immune system
22	43.8	2.5	18997	24	ABL32570	Human immune system
23	43.4	2.5	9510	22	AAZ46438	Human immune system
24	43.4	2.5	9510	24	ABL34563	Tumour suppressor
25	43.2	2.5	6261	22	AAZ46643	Human metastasis
26	43.2	2.5	6261	22	AAZ61046	Tumour suppressor
27	43.2	2.5	15853	24	AAZ61456	Human gene regulator
28	42.6	2.4	4590	22	AAZ42065	Human gene regulator
29	42.6	2.4	34769	22	AAZ46775	Yeast AOP604-asso
30	42.2	2.4	11726	22	ABL34063	Tumour suppressor
31	42.2	2.4	12025	24	ABL33299	Human immune system
32	42.2	2.4	15282	24	AAZ61139	Human immune system
33	41.6	2.4	8305	24	ABL33569	Human gene regulator
34	41.6	2.4	12138	24	ABL33629	Human immune system
35	41.6	2.4	335913	22	AAZ61371	Human immune system
36	41.6	2.4	335913	22	AAZ61372	Soybean 240017 reg
37	41.4	2.4	1183	19	AAZ9583	Soybean 240017 reg
38	41.2	2.3	10619	22	AAZ54236	Pythium oligandrum
39	41.2	2.3	10619	24	ABL32070	Chemically induced
40	41.2	2.3	10886	24	ABL34135	Human immune system
41	41.2	2.3	40862	24	ABL34073	Human immune system
42	41	2.3	6475	24	ABL34248	Human immune system
43	41	2.3	13814	24	ABL33192	Human immune system
44	40.8	2.3	6587	24	ABL32384	Human immune system
45	40.4	2.3	6207	22	AAZ46777	Tumour suppressor

#### ALIGNMENTS

RESULT 1  
AAZ52234  
ID AAZ52234 standard; DNA; 1760 BP.  
AC AAZ52234;  
XX  
DT 18-JUL-2000 (first entry)  
DE Maize glycine-rich protein 3 gene 5' regulatory element #1.  
XX  
KW Maize; glycine-rich protein 3; GRP3; 5' regulatory element;  
KW root specific gene expression; root abundant gene; monooctyladen;  
KW pathogen resistance; pest; herbicide; growth rate; ds.  
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OS Zea mays.  
XX  
FH Key  
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XX  
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XX  
XX 11-SEP-1998; 98EP-0117251.  
XX  
XX (AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.  
XX  
XX Felix G. Wulff D;

XX WPI: 2000-271382/23.  
XX Nucleic acid sequence is used for cloning and expressing a root  
PT specific or root abundant gene in a plant -  
XX  
PS Claim 1; Page 49-50; 60pp; English.  
XX  
CC The present sequence is a 5' regulatory element of maize glycine-rich  
CC protein 3 (GRP3) gene. It corresponds to positions 1-1760 of the partial  
CC genomic clone zmGRP3. The present sequence is useful for cloning and  
CC expressing root specific or root abundant genes in plants, especially  
CC monocots which provide high expression efficiency and high  
CC tissue specificity. Root preferred gene expression provides several  
CC advantages to plants e.g. resistance to pathogens, pests, herbicides and  
CC adverse weather conditions, modification of growth rate and alteration of  
CC root tissue function. This sequence also provides a means of isolating  
CC related regulatory sequences of other plant species which confer root  
CC specificity to genes of interest operably linked to them.  
XX  
SQ Sequence 1760 BP; 433 A; 461 C; 414 G; 452 T; 0 other;

Query Match 100.0%; Score 1760; DB 21; Length 1760;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1760; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1201 aaatttagatctcgtctcgttcgaacagatagactatacccttcggttgggtgagattagc 1260  
QY 1261 aactagaanaattatggtcctcatgtgtcttcttgcgcctcctcaaaatttcgtcctgcg 1320  
DB 1261 aactagaanaattatggtcctcatgtgtcttcttgcgcctcctcaaaatttcgtcctgcg 1320  
QY 1321 tccgcacactatagctgctgcggaggtgcggggtacggtatcgtgtaactctgaagtcgaacag 1380  
DB 1321 tccgcacactatagctgctgcggaggtgcggggtacggtatcgtgtaactctgaagtcgaacag 1380  
QY 1381 tgatggttactatctaatatggtcccggtcagtaataataactgttgcgacgaatggaaatct 1440  
DB 1381 tgatggttactatctaatatggtcccggtcagtaataataactgttgcgacgaatggaaatct 1440  
QY 1441 ctagttttgacagaanaacgaagcgaactgtctatgtctaaacttaattccagagagatcga 1500  
DB 1441 ctagttttgacagaanaacgaagcgaactgtctatgtctaaacttaattccagagagatcga 1500  
QY 1501 ttcttacaagtctagctgcaacaaatcgaatgtgcatcagaacgatatatgctaatgg 1560  
DB 1501 ttcttacaagtctagctgcaacaaatcgaatgtgcatcagaacgatatatgctaatgg 1560  
QY 1561 ttcttcttatcagatagctgtgcaacaaatgtgcatcagaatcagaagtctcttcgccttga 1620  
DB 1561 ttcttcttatcagatagctgtgcaacaaatgtgcatcagaatcagaagtctcttcgccttga 1620  
QY 1621 tccgatactcatcagacatgtgacacccaatcttgcacaaacgagcggggggaaacccgaa 1680  
DB 1621 tccgatactcatcagacatgtgacacccaatcttgcacaaacgagcggggggaaacccgaa 1680  
QY 1681 acatcgcgtccatgtcaacagccccaagcaggtataataataccatgcaatgtcaatgcaagcg 1740  
DB 1681 acatcgcgtccatgtcaacagccccaagcaggtataataataccatgcaatgtcaatgcaagcg 1740  
QY 1741 ggtcatcatcatgcaactcca 1760  
DB 1741 ggtcatcatcatgcaactcca 1760

RESULT	2
AAZ52247	
ID	AAZ52247 standard; DNA; 3416 BP.
XX	
AC	
XX	AAZ52247;
DT	18-JUL-2000 (first entry)
DE	
XX	
XX	Maize glycine-rich protein 3 partial genomic clone zmGRP3.
KW	
KW	Maize; glycine-rich protein 3; GRP3; regulatory element; zmGRP3;
KW	root specific gene expression; root abundant gene; monocotyledon;
KW	pathogen resistance; pest; herbicide; growth rate; ds.
OS	
XX	Zea mays. `
FH	
FT	Key
FT	promoter
FT	Location/Qualifiers
FT	1..1780
FT	/tag= a
FT	TATA_signal
FT	1712..1719
FT	/tag= b
FT	CDS
FT	1781..2560
FT	/tag= c
FT	/product= "GRP3"
FT	/note= "Glycine-rich protein 3"
FT	misc_signal
FT	2561..3416
FT	/tag= d
FT	/label= 3',_regulatory_element
FT	polyA_signal
FT	2692..2696
FT	/tag= e
FN	
XX	WO200015662-A1.
XX	
PD	23-MAR-2000.
XX	
PF	10-SEP-1999; 99WO-EP06692.
XX	
PR	11-SEP-1998; 98EP-0117251.
XX	
PA	(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.
XX	
PI	Felix G, Wulff D;
DR	
XX	WPI: 2000-271382/23.
XX	
PT	Nucleic acid sequence is used for cloning and expressing a root
PT	specific or root abundant gene in a plant -
XX	
PS	Claim 4; Page 55-56; 60pp; English.
XX	
CC	The present sequence is a partial genomic clone zmGRP3 encoding
CC	maize glycine-rich protein 3 (GRP3). This sequence comprises 5' and
CC	3' regulatory elements useful for cloning and
CC	expressing root specific or root abundant genes in plants, especially
CC	monocots which provide high expression efficiency and high
CC	tissue specificity. Root preferred gene expression provides several
CC	advantages to plants e.g. resistance to pathogens, pests, herbicides and
CC	adverse weather conditions, modification of growth rate and alteration of
CC	root tissue function. This sequence also provides a means of isolating
CC	related regulatory sequences of other plant species which confer root
CC	specificity to genes of interest operably linked to them.
QX	
Sequence	3416BP; 755 A; 841 C; 950 G; 870 T; 0 other;

Query Match	100.0%	Score 1760;	DB 21;	Length 3416;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1760;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	ctcgagatgttgatagagaggaatttcgagcaaccgagctctcaagcagcccaag	60	

Db	1	ctcgagatggttggataagaagaaggaatttgcgcagcaaccgagatctccaaggacgcgcaacg	60
QY	61	cgacatctcgcgagtgagtgagtgctcgctgaatgttcgcagaaagagagctctgattgttcgcgat	120
Db	61	cgacatctcgcgagtgagtgagtgctcgctgaatgttcgcagaaagagagctctgattgttcgcgat	120
QY	121	cgcgagcttcagatttggctctccatgagccccaagatgttttggcgcgcgcgctgttaatgagc	180
Db	121	cgcgagcttcagatttggctctccatgagccccaagatgttttggcgcgcgcgctgttaatgagc	180
QY	181	agacgcgcagaccgcgagacccggtgtctccgatccaattgtttgaacaatlagcacgcgcgcaag	240
Db	181	agacgcgcagaccgcgagacccggtgtctccgatccaattgtttgaacaatlagcacgcgcgcaag	240
QY	241	cagcgcaacaatcccgagagacaataatttgggggagagcagataagcttggagaggaag	300
Db	241	cagcgcaacaatcccgagagacaataatttgggggagagcagataagcttggagaggaag	300
QY	301	aacaaatgacagcagtgatattctctctctgtctccctctgttaaccctctccaattaat	360
Db	301	aacaaatgacagcagtgatattctctctctgtctccctctgttaaccctctccaattaat	360
QY	361	actccattacaaggtcggcccaacagcgacccacgctcggtgtccacgaaacttggat	420
Db	361	actccattacaaggtcggcccaacagcgacccacgctcggtgtccacgaaacttggat	420
QY	421	gggttttggcgagcgacgacgtgtctctgtcgcgagctctgtctgtgagctgt	480
Db	421	gggttttggcgagcgacgacgtgtctctgtcgcgagctctgtctgtgagctgt	480
QY	481	gctcgcgctgtctaaacatctcttcttcttggcagcagctctgcgttggcagcggttaact	540
Db	481	gctcgcgctgtctaaacatctcttcttcttggcagcagctctgcgttggcagcggttaact	540
QY	541	ggcgctctgctcaaaagaatttgcctacagatgcctgagcgttcagctcgacgagcgttgaatcc	600
Db	541	ggcgctctgctcaaaagaatttgcctacagatgcctgagcgttcagctcgacgagcgttgaatcc	600
QY	601	gaggttcgcgaatagcagcgaacgctgaagctgcatgctgtacacggctcttaataaacg	660
Db	601	gaggttcgcgaatagcagcgaacgctgaagctgcatgctgtacacggctcttaataaacg	660
QY	661	agctctactcgctacgttgaactatagcacaacagcgatccacaggggggccaagta	720
Db	661	agctctactcgctacgttgaactatagcacaacagcgatccacaggggggccaagta	720
QY	721	ggccatggccccccctcaatttggtaacccttttaactaagtattttagatataa	780
Db	721	ggccatggccccccctcaatttggtaacccttttaactaagtattttagatataa	780
QY	781	gtgtagaanaaalccaataattttagatgtataaanaatctgttcttaaatctctaaacta	840
Db	781	gtgtagaanaaalccaataattttagatgtataaanaatctgttcttaaatctctaaacta	840
QY	841	ataaactgttggctaaantttggccaanaaggttttagaatgataccaactattgttagctata	900
Db	841	ataaactgttggctaaantttggccaanaaggttttagaatgataccaactattgttagctata	900
QY	901	ccctttaaataagatataattttagatgtggcccaacctgctaaacccggttaacagtta	960
Db	901	ccctttaaataagatataattttagatgtggcccaacctgctaaacccggttaacagtta	960
QY	961	gctctagatgtttagaacaatgctccaaacaacataattagagcctatcgcgcgagatct	1020
Db	961	gctctagatgtttagaacaatgctccaaacaacataattagagcctatcgcgcgagatct	1020
QY	1021	ctcggttccagctccagatcattaccagttcgtactctaatcttccgcgacacacctaaca	1080
Db	1021	ctcggttccagctccagatcattaccagttcgtactctaatcttccgcgacacacctaaca	1080
QY	1081	gtctgctcgcgtccgttcttcgcgcaacgcgacatctcccgatgcgcgttcaaccgagattc	1140
Db	1081	gtctgctcgcgtccgttcttcgcgcaacgcgacatctcccgatgcgcgttcaaccgagattc	1140

QY	1141	gcccttcgtagaagcgtccgtcccttgctccggtttttctctgtgaagtcgtacgcgtcag	1200
Db	1141	gcccttcgtagaagcgtccgtcccttgctccggtttttctctgtgaagtcgtacgcgtcag	1200
QY	1201	aaattgaatctgcctcgtgcgaacgatatgaatttcccttcggtcgctggtagacttgag	1260
Db	1201	aaattgaatctgcctcgtgcgaacgatatgaatttcccttcggtcgctggtagacttgag	1260
QY	1261	aactagaanaattatggtctccatgctgctctttcttttggccctccctaatttgccttcg	1320
Db	1261	aactagaanaattatggtctccatgctgctctttcttttggccctccctaatttgccttcg	1320
QY	1321	tcgcgcactctatagctcgcggggtgtcggggtatccgttatccgtgaatctcgaagtcgaag	1380
Db	1321	tcgcgcactctatagctcgcggggtgtcggggtatccgttatccgtgaatctcgaagtcgaag	1380
QY	1381	tgaatgcgtactatcatgtgccgcgtcagtaataatcattgtttcccgacgatalggaatct	1440
Db	1381	tgaatgcgtactatcatgtgccgcgtcagtaataatcattgtttcccgacgatalggaatct	1440
QY	1441	ctagttttgacagaagaacgaagcaactgtctatgtctagctaatatctccagagagatcga	1500
Db	1441	ctagttttgacagaagaacgaagcaactgtctatgtctagctaatatctccagagagatcga	1500
QY	1501	ttttcacagtgctagctgcgcacaacatcgatggcaattggcatcgcagagatatatgtcaatcg	1560
Db	1501	ttttcacagtgctagctgcgcacaacatcgatggcaattggcatcgcagagatatatgtcaatcg	1560
QY	1561	ttttcttatacgtatcgctgtgttcaacagctgcgataccagatataagagttctctcgcctga	1620
Db	1561	ttttcttatacgtatcgctgtgttcaacagctgcgataccagatataagagttctctcgcctga	1620
QY	1621	tcgatatctatcgcaatggaacacccaatctgtccaaacccagcggggcggggaaaccgaa	1680
Db	1621	tcgatatctatcgcaatggaacacccaatctgtccaaacccagcggggcggggaaaccgaa	1680
QY	1681	acatcgcgctcatgacgagccccacgacgataataatcccatgcaatgcatgcaagc	1740
Db	1681	acatcgcgctcatgacgagccccacgacgataataatcccatgcaatgcatgcaagc	1740
QY	1741	ggtcatcatcatcatgcatcga	1760
Db	1741	ggtcatcatcatcatgcatcga	1760
RESULT 3			
ID	AA52244	standard; DNA; 1710 BP.	
XX	AA52244;		
AC			
XX	18-JUL-2000	(first entry)	
DE			
XX		Maize glycine-rich protein 3 gene 5' regulatory element #11.	
XX		Maize; glycine-rich protein 3; GRP3; 5' regulatory element;	
KM		root specific gene expression; root abundant gene; monocotyledon;	
KW		pathogen resistance; pest; herbicide; growth rate; ds.	
XX			
OS		Zea mays.	
PN		MO200015662-A1.	
PD		23-MAR-2000.	
XX			
PF		10-SEP-1999; 99WO-EP06692.	
XX			
PR		11-SEP-1998; 98EP-0117251.	
XX			
PA		(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.	
PI		Feix G, Wulff D;	
XX			

XX WP1: 2000-271382/23.  
XX  
XX Nucleic acid sequence is used for cloning and expressing a root  
PT specific or root abundant gene in a plant -  
XX  
XX  
PS  
XX Claim 3; Page 54; 60pp; English.  
XX  
CC The present sequence is a 5' regulatory element of maize glycine-rich  
CC protein 3 (GRP3) gene. It corresponds to positions 1-1710 of the  
CC partial genomic clone zmGRP3. The present sequence is useful for cloning  
CC and expressing root specific or root abundant genes in plants,  
CC and especially monocots which provide high expression efficiency and high  
CC tissue specificity. Root preferred gene expression provides several  
CC advantages to plants e.g. resistance to pathogens, pests, herbicides and  
CC adverse weather conditions, modification of growth rate and alteration of  
CC root tissue function. This sequence also provides a means of isolating  
CC related regulatory sequences of other plant species which confer root  
CC specificity to genes of interest operably linked to them.  
XX  
XX Sequence 1710 BP; 417 A; 446 C; 406 G; 441 T; 0 other;  
SQ

Query	Match	Similarity	97.2%	Score	1710:	DB	21:	Length	1710:
Best	Local	Similarity	100.0%	Pred.	No.	0:			
Matches	1710:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
QY	1	ctcgaagatcttgatagaagagaatttcgacacacgaggtctccaaaggcagccacag	60						
Db	1	ctcgaagatgcttgatagaagagaatttcgacacacgaggtctccaaaggcagccacag	60						
QY	61	cgcatctcgcgcagtgaggtggtgcctgagtcgcgcgaagagattcgtatctgcgat	120						
Db	61	cgcatctcgcgcagtgaggtggtgcctgagtcgcgcgaagagattcgtatctgcgat	120						
QY	121	cgcgaagcttcagatttgggtctcatccatcccaattgtttgggcgcgcgtttaatgac	180						
Db	121	cgcgaagcttcagatttgggtctcatccatcccaattgtttgggcgcgcgtttaatgac	180						
QY	181	agacgcagacaccgagaccggtgctccgataccaattgtttaagcaatagcagcggaacag	240						
Db	181	agacgcagacaccgagaccggtgctccgataccaattgtttaagcaatagcagcggaacag	240						
QY	241	cagcgagacacatccgagagacatagttttggggagagacagcatagctttgagagggagaaag	300						
Db	241	cagcgagacacatccgagagacatagttttggggagagacagcatagctttgagagggagaaag	300						
QY	301	aacaaatagtagacagcgttaagatctctctcgtgctccctctgttaacctctcaatctaact	360						
Db	301	aacaaatagtagacagcgttagatctctctcgtgctccctctgttaacctctcaatctaact	360						
QY	361	actccctataacaaagtcgcgcgccatacgaagcgagaccacgctgcggtttccacgaacttggatt	420						
Db	361	actccctataacaaagtcgcgcgccatacgaagcgagaccacgctgcggtttccacgaacttggatt	420						
QY	421	gggtctgtgcgcgcgcgcgcgcgtgtctctgcctcgtctgcgttgagcttctcgtggagctgtt	480						
Db	421	gggtctgtgcgcgcgcgcgcgcgtgtctctgcctcgtctgcgttgagcttctcgtggagctgtt	480						
QY	481	gctcgcgcgtgcttaacaatctctgttgtttgttggaagacttcgcgtggtggccaacggttaact	540						
Db	481	gctcgcgcgtgcttaacaatctctgttgtttgttggaagacttcgcgtggtggccaacggttaact	540						
QY	541	ggcctctgctcaagaagaattgacctatacagtgctcgtgcgcgttcgaacgcgttgaaacc	600						
Db	541	ggcctctgctcaagaagaattgacctatacagtgctcgtgcgcgttcgaacgcgttgaaacc	600						
QY	601	gaagtcgcgcagtaacgaggaacacgctgagctgcatactgttaccggcttattataactg	660						
Db	601	gaagtcgcgcagtaacgaggaacacgctgagctgcatactgttaccggcttattataactg	660						
QY	661	agctctactcgcgtacttgatctaataagcaccacgaagcgagatccagaggggggccaagta	720						

Dh 661 agcttactcgtactagctatagcgaccagagcgcatccagaggcggaagta 720  
QY 721 ggcattggccccctcaatttgtacacccctttatataccaaatgattattagattaa 780  
Dh 721 ggcattggccccctcaatttgtacacccctttatataccaaatgattattagattaa 780  
QY 781 gtgtagaanaaatcaaaattttagataatataaaatctgttccaaatccttaaaacta 840  
Dh 781 gtgtagaanaaatcaaaattttagataatataaaatctgttccaaatccttaaaacta 840  
QY 841 atagctgtgtctaaataatagccaaaagtttagaalygaatcaactaatgtttagctata 900  
Dh 841 atagctgtgtctaaataatagccaaaagtttagaalygaatcaactaatgtttagctata 900  
QY 901 ccccttaataagattaatgtttagagggcccaaccagtaaacagtaaacagta 960  
Dh 901 ccccttaataagattaatgtttagagggcccaaccagtaaacagtaaacagta 960  
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Dh 961 gctctagatgtttagaacaatgacctaaacaacatattatagcctactgcggaatcct 1020  
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Dh 1021 ctgagttcagttcctagatcctaacagttcgtactaaatctccgacaaccaataacca 1080  
QY 1081 gtctgctcgtcgtccctgtttccgacacgaccatctccgaatgagaagtaacccgacttc 1140  
Dh 1081 gtctgctcgtcgtccctgtttccgacacgaccatctccgaatgagaagtaacccgacttc 1140  
QY 1141 gccctctgtagcgccctcgtccctgttccctgttcttctcgtgacgtcgcgactcgac 1200  
Dh 1141 gccctctgtagcgccctcgtccctgttccctgttcttctcgtgacgtcgcgactcgac 1200  
QY 1201 aaattagatctgctcgtcgcgaagaataaactatccctcgtcgtcgtgagttgacttga 1260  
Dh 1201 aaattagatctgctcgtcgcgaagaataaactatccctcgtcgtcgtgagttgacttga 1260  
QY 1261 aaactagaanaattatgctcctcatgtgtcttcttggccctcccaaaatttgcgcgcg 1320  
Dh 1261 aaactagaanaattatgctcctcatgtgtcttcttggccctcccaaaatttgcgcgcg 1320  
QY 1321 tccgcaactctatagctgcgggagtgcggggtacgtaatcgtgaatcgtgaatcgaacag 1380  
Dh 1321 tccgcaactctatagctgcgggagtgcggggtacgtaatcgtgaatcgtgaatcgaacag 1380  
QY 1381 tgaatgagtaactatcctaaatgtcccgtagcaataataatcgttgcgacagatgggaatct 1440  
Dh 1381 tgaatgagtaactatcctaaatgtcccgtagcaataataatcgttgcgacagatgggaatct 1440  
QY 1441 ctgattttgacagaanaacgaagcaactgctatgcttagctaatcaattccagagagatcga 1500  
Dh 1441 ctgatttttgcagagaanaacgaagcaactgctatgcttagctaatcaattccagagagatcga 1500  
QY 1501 tttctctacagtgctagctgcaacaaatcgaatgtgcatcagaagatatagctaaatg 1560  
Dh 1501 tttctctacagtgctagctgcaacaaatcgaatgtgcatcagaagatatagctaaatg 1560  
QY 1561 tttctcttaacgaatcgttgcacagtgtagatcgaatcaagagttctctcgccttga 1620  
Dh 1561 tttctcttaacgaatcgttgcacagtgtagatcgaatcaagagttctctcgccttga 1620  
QY 1621 tccgagatcctacatgagacacccatctgcgaacccagcgggcgagggaacccgaa 1680  
Dh 1621 tccgagatcctacatgagacacccatctgcgaacccagcgggcgagggaacccgaa 1680  
QY 1681 acatcgcggtccatgacgagaccccaacgag 1710  
Dh 1681 acatcgcggtccatgacgagaccccaacgag 1710

RESULT 4  
AA52243

1D AA52243 standard; DNA; 1550 BP.  
XX  
AC AA52243;  
XX  
DT 18-JUL-2000 (first entry)  
XX  
DE Maize glycine-rich protein 3 gene 5' regulatory element #10.  
XX  
KW Maize; glycine-rich protein 3; GRP3; 5' regulatory element;  
RV root specific gene expression; root abundant gene; monocotyledon;  
XX pathogen resistance; pest; herbicide; growth rate; ds.  
OS Zea mays.  
XX  
PN W0200015662-A1.  
PD 23-MAR-2000.  
XX  
PF 10-SEP-1999; 99WO-EP06692.  
XX  
PR 11-SEP-1998; 98EP-0117251.  
XX  
PA (AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.  
XX  
PI Felix G. Wulff D;  
XX  
DR WPI; 2000-271382/23.  
XX  
PT Nucleic acid sequence is used for cloning and expressing a root  
PS specific or root abundant gene in a plant -  
XX  
XX Claim 3; Page 53-54; 60pp; English.  
XX  
CC The present sequence is a 5' regulatory element of maize glycine-rich  
CC protein 3 (GRP3) gene. It corresponds to positions 1-1550 of the  
CC partial genomic clone zmGRP3. The present sequence is useful for cloning  
CC and expressing root specific or root abundant genes in plants,  
CC especially monocots which provide high expression efficiency and high  
CC tissue specificity. Root preferred gene expression provides several  
CC advantages to plants e.g. resistance to pathogens, pests, herbicides and  
CC adverse weather conditions, modification of growth rate and alteration of  
CC root tissue function. This sequence also provides a means of isolating  
CC related regulatory sequences of other plant species which confer root  
CC specificity to genes of interest operably linked to them.  
SQ  
Sequence 1550 BP; 379 A; 394 C; 369 G; 408 T; 0 other;  
Query Match 88.1%; Score 1550; DB 21; Length 1550;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ctgagatgttgaatagaagaagaattgcgagcaacgagttctcaagcgacccaag 60  
Dh 1 ctgagatgttgaatagaagaagaattgcgagcaacgagttctcaagcgacccaag 60  
QY 61 cgcactctgcgcagtgagtggtgcgtcgtatgctgcgagaagagcttcgattgttcgat 120  
Dh 61 cgcactctgcgcagtgagtggtgcgtcgtatgctgcgagaagagcttcgattgttcgat 120  
QY 121 cgcagctcagatttggctccatgaccccaagattgttggcggcgcgctgtatagc 180  
Dh 121 cgcagctcagatttggctccatgaccccaagattgttggcggcgcgctgtatagc 180  
QY 181 agacgcagaccgcgagacgggtctccgatalaccaatgtttagcaatagcagcgacaag 240  
Dh 181 agacgcagaccgcgagacgggtctccgatalaccaatgtttagcaatagcagcgacaag 240  
QY 241 cagcgacaacatccgagagaatagtttggggggagcaaatagcttgggaggaagaag 300  
Dh 241 cagcgacaacatccgagagaatagtttggggggagcaaatagcttgggaggaagaag 300  
QY 301 aacaatagtgacagcgtagattctctctgtctcctctgttaacccctctcaatcaat 360

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Db      301 aacaaatgtaagcgtatattccctctctgtctctctgttaacctctctcaatcaat 360
      361 actccatatacaaggctcgcccatcaagcgcaaccagtcgaggtccaagaacttggatt 420
      361 actccatatacaaggctcgcccatcaagcgcaaccagtcgaggtccaagaacttggatt 420
      421 ggggttgtagcagcgcgcagctgttcttgctctgttgagtgctgtctgttgagtgct 480
      421 ggggttgtagcagcgcgcagctgttcttgctctgttgagtgctgtctgttgagtgct 480
      481 gctcgcgcgtaacaacatctctgtgttcttgcaagacttcgctgcaagcggttaact 540
      481 gctcgcgcgtaacaacatctctgtgttcttgcaagacttcgctgcaagcggttaact 540
      541 ggcgtctgtccaagaanaattgcctatacagtcgcctgagtcagctcagagcggttaacc 600
      541 ggcgtctgtccaagaanaattgcctatacagtcgcctgagtcagctcagagcggttaacc 600
      601 gaggctcgcaagtagcagcgcaaacgctgagctgcatgctgttaaccggttataatactg 660
      601 gaggctcgcaagtagcagcgcaaacgctgagctgcatgctgtgttaaccggttataatactg 660
      661 agctctactcgcgaagctagctatagcagccacagagcgagatccagaggggggcaagta 720
      661 agctctactcgcgaagctagctatagcagccacagagcgagatccagaggggggcaagta 720
      721 ggcacatgccccccccaatttctgtacaacctttatacctaattgattatttattata 780
      721 ggcacatgccccccccaatttctgtacaacctttatacctaattgattatttattata 780
      781 ggtgtagaaaaaacaaattttagatagatataaaatctgtctctaactctcaaaacta 840
      781 ggtgtagaaaaaacaaattttagatagatataaaatctgtctctaactctcaaaacta 840
      841 atagctagtgctcaaaatttagcacaagaagtttagaatggaatcaactaatgttagctata 900
      841 atagctagtgctcaaaatttagcacaagaagtttagaatggaatcaactaatgttagctata 900
      901 ccccttaaaaataattatattgtttagatgcccacaactagctaaacaaatcaacattta 960
      901 ccccttaaaaataattatattgtttagatgcccacaactagctaaacaaatcaacattta 960
      961 gctctagatgtttagaacaatgagcctaacaacataattatgagcctactcgcgagtcct 1020
      961 gctctagatgtttagaacaatgagcctaacaacataattatgagcctactcgcgagtcct 1020
      1021 ctgagttcagtcctatgatactaccagtcgactctaattctcccgacaacactaaacca 1080
      1021 ctgagttcagtcctatgatactaccagtcgactctaattctcccgacaacactaaacca 1080
      1081 gttctgcgtgctgcctgtttccgcgcaacgacccattcccgatggaagtaaccgacttcc 1140
      1081 gttctgcgtgctgcctgtttccgcgcaacgacccattcccgatggaagtaaccgacttcc 1140
      1141 gccctctgtagcgctccgctccctgtctctgttttctcgtgagtcgataccgctcgac 1200
      1141 gccctctgtagcgctccgctccctgtctctgttttctcgtgagtcgataccgctcgac 1200
      1201 aaattagatctcgtctgtagcaagaatagatactatccctctgagtggtgagatttagc 1260
      1201 aaattagatctcgtctgtagcaagaatagatactatccctctgagtggtgagatttagc 1260
      1261 aactagaanaattatggtctcagtcgtctttttgagccctcccaaaatttctgcctgcg 1320
      1261 aactagaanaattatggtctcagtcgtctttttgagccctcccaaaatttctgcctgcg 1320
      1321 tccgcaactctatagctgcgggagtgcggggtacagtcacgtacatcgtgaagtgcgaacag 1380
      1321 tccgcaactctatagctgcgggagtgcggggtacagtcacgtacatcgtgaagtgcgaacag 1380
      1381 tgataggtactatctaatgcccgtgtagtaataactgttgcgagcgatgggaatct 1440
      1381 tgataggtactatctaatgcccgtgtagtaataactgttgcgagcgatgggaatct 1440

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Db      1381 tgatgcgctactatactaatgctccgctgcaagtaataactgttgcgagcagtggaatct 1440
      1441 ctagttttagacaagaacgaaggaactgctatgtagtaactaatattccaagagatacga 1500
      1441 ctagttttagacaagaacgaaggaactgctatgtagtaactaatattccaagagatacga 1500
      1501 ttctcaagtgctagctgcaacaatcagatgcgaatttggcatcagaagatat 1550
      1501 ttctcaagtgctagctgcaacaatcagatgcgaatttggcatcagaagatat 1550

```

RESULT 5  
AA52242  
ID AA52242 standard; DNA; 1497 BP.

AA52242;  
18-JUL-2000 (first entry)

Maize glycine-rich protein 3 gene 5' regulatory element #9.

Maize: glycine-rich protein 3; GRP3; 5' regulatory element;  
root specific gene expression; root abundant gene; monocotyledon;  
pathogen resistance; pest; herbicide; growth rate; ds.

Zea mays.

MO200015662-A1.

23-MAR-2000.

10-SEP-1999; 99MO-EP06692.

11-SEP-1998; 98EP-0117251.

(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.

Feix G, Muller D;

WPI; 2000-271382/23.

Nucleic acid sequence is used for cloning and expressing a root  
specific or root abundant gene in a plant -

Claim 3; Page 53; 60pp; English.

The present sequence is a 5' regulatory element of maize glycine-rich  
protein 3 (GRP3) gene. It corresponds to positions 1-1497 of the  
partial genomic clone zmGRP3. The present sequence is useful for cloning  
and expressing root specific or root abundant genes in plants,  
especially monocots which provide high expression efficiency and high  
tissue specificity. Root preferred gene expression provides several  
advantages to plants e.g. resistance to pathogens, pests, herbicides and  
adverse weather conditions, modification of growth rate and alteration of  
root tissue function. This sequence also provides a means of isolating  
CC related regulatory sequences of other plant species which confer root  
specificity to genes of interest operably linked to them.

Sequence 1497 BP; 363 A; 382 C; 358 G; 394 T; 0 other;

Query Match 85.1%; Score 1497; DB 21; Length 1497;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ctgagatgttggatagaagaagatgagcaacgaggtctccaagcgacccaag 60

1 ctgagatgttggatagaagaagatgagcaacgaggtctccaagcgacccaag 60

61 cgcacctcgcaagtgaggtgctcgatgctcggaagagcttgattgttgcat 120

61 cgcacctcgcaagtgaggtgctcgatgctcggaagagcttgattgttgcat 120

QY 121 cgcgagctcagatttgctccatgaccccaagatctgtttgycgcgcgtgttaatgagc 180  
DB 121 cgcgagctcagatttgctccatgaccccaagatctgtttgycgcgcgtgttaatgagc 180  
QY 181 agagcccgagcccgagaccggtgtctccgataccaattggttagcaatagcaagcaag 240  
DB 181 agagcccgagcccgagaccggtgtctccgataccaattggttagcaatagcaagcaag 240  
QY 241 cagcgaaacatccgagacacatagtttggggagagacagatagtttgaagggagagag 300  
DB 241 cagcgaaacatccgagacacatagtttggggagagacagatagtttgaagggagagag 300  
QY 301 aacaatagtgacagctgattctctctgtctctgttaccctctcctaactat 360  
DB 301 aacaatagtgacagctgattctctctgtctctgttaccctctcctaactat 360  
QY 361 actcctattacaaggtcgcccatagcgaccccgagcccgagtcgcggttccacgaacttggagt 420  
DB 361 actcctattacaaggtcgcccatagcgaccccgagtcgcggttccacgaacttggagt 420  
QY 421 gggatttgtcgagccgagctgcttctgtctgtgagatctgtctgttggagctgtt 480  
DB 421 gggatttgtcgagccgagctgcttctgtctgtgagatctgtctgttggagctgtt 480  
QY 481 gctcgcgctgtcaacaatctctgttgttgcagacactcgcgtgycacgcgttaact 540  
DB 481 gctcgcgctgtcaacaatctctgttgttgcagacactcgcgtgycacgcgttaact 540  
QY 541 ggcctctgcctcaagaattgcctatacagtcgctggcgtaagctgcacgagcttgaaacc 600  
DB 541 ggcctctgcctcaagaattgcctatacagtcgctggcgtaagctgcacgagcttgaaacc 600  
QY 601 gaagtcgcagtagcagagcaaacgctgagctgcatactgcataccgcttataactaactg 660  
DB 601 gaagtcgcagtagcagagcaaacgctgagctgcatactgcataccgcttataactaactg 660  
QY 661 agcctactgcctagctagtatagtagcacaagggcgagatccagagggggcaagta 720  
DB 661 agcctactgcctagctagtatagtagcacaagggcgagatccagagggggcaagta 720  
QY 721 ggcacatggcccccctcaattttgtacaccccttataccctaagattatagattaa 780  
DB 721 ggcacatggcccccctcaattttgtacaccccttataccctaagattatagattaa 780  
QY 781 gtgtagaaaaatacaaaattttagatagtagtaaaaatctgttctaactctaacta 840  
DB 781 gtgtagaaaaatacaaaattttagatagtagtaaaaatctgttctaactctaacta 840  
QY 841 atagctagttgctaaaatttagccaaaaggttagaagtagcaactaattgttagctata 900  
DB 841 atagctagttgctaaaatttagccaaaaggttagaagtagcaactaattgttagctata 900  
QY 901 ccccttaataatgatttaattgttagatggccaacctagctaaacacgaagtaacagta 960  
DB 901 ccccttaataatgatttaattgttagatggccaacctagctaaacacgaagtaacagta 960  
QY 961 gctctagaattttagaacaatggcctaaacaacatattatagcctactcgcgcagatcct 1020  
DB 961 gctctagaattttagaacaatggcctaaacaacatattatagcctactcgcgcagatcct 1020  
QY 1021 ctgcgttcagctcagagatttccagctgacttaatttcccgaaacacccctaaacca 1080  
DB 1021 ctgcgttcagctcagagatttccagctgacttaatttcccgaaacacccctaaacca 1080  
QY 1081 gctcgtcgtcgtccctgttttcgcgacacgacccatctccgagtagcagctcaccgacttc 1140  
DB 1081 gctcgtcgtcgtccctgttttcgcgacacgacccatctccgagtagcagctcaccgacttc 1140  
QY 1141 gccocctcgtagcgccctcgcctcgttctcgttcttcgttgacgtcgatccgctgac 1200  
DB 1141 gccocctcgtagcgccctcgcctcgttctcgttcttcgttgacgtcgatccgctgac 1200  
QY 1201 aaattagatctcgtctgcgacaagatagctatccctcgtcgtcggtgagattgagc 1260

DB 1201 aaattagatctcgtctgcgacaagatagctatccctcgtcgcgtcggtgagattgagc 1260  
QY 1261 aactagaataatatygtctcaltggttcttggccctcctaatttgcctcgcg 1320  
DB 1261 aactagaataatatygtctcaltggttcttggccctcctaatttgcctcgcg 1320  
QY 1321 tccgcacactatagctgtaggagtgtagcgtgacccgtatcgtgaatcgtgaacag 1380  
DB 1321 tccgcacactatagctgtaggagtgtagcgtgacccgtatcgtgaatcgtgaacag 1380  
QY 1381 tgatgagctacatctaatgctccgtgcagtaatactactgttgcagagatgggaatct 1440  
DB 1381 tgatgagctacatctaatgctccgtgcagtaatactactgttgcagagatgggaatct 1440  
QY 1441 ctgattttgacagaacaagcaagcagctgatactgtagctaatatccagaagat 1497  
DB 1441 ctgattttgacagaacaagcaagcagctgatactgtagctaatatccagaagat 1497

RESULT 6

AAZ52241 standard; DNA; 1354 BP.

AAZ52241;

18-JUL-2000 (first entry)

Maize glycine-rich protein 3 gene 5' regulatory element #8.

Maize; glycine-rich protein 3; GRP3; 5' regulatory element;

root specific gene expression; root abundant gene; monootyledon;

pathogen resistance; pest; herbicide; growth rate; ds.

Zea mays.

W0200015662-A1.

23-MAR-2000.

10-SEP-1999; 99WO-EP06692.

11-SEP-1998; 98EP-0117251.

(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.

Felix G. Wulff D;

Nucleic acid sequence is used for cloning and expressing a root

specific or root abundant gene in a plant -

Claim 3; Page 52; 60pp; English.

The present sequence is a 5' regulatory element of maize glycine-rich protein 3 (GRP3) gene. It corresponds to positions 1-1354 of the partial genomic clone zmGRP3. The present sequence is useful for cloning and expressing root specific or root abundant genes in plants, especially monocots which provide high expression efficiency and high tissue specificity. Root preferred gene expression provides several advantages to plants e.g. resistance to pathogens, pests, herbicides and adverse weather conditions, modification of growth rate and alteration of root tissue function. This sequence also provides a means of isolating related regulatory sequences of other plant species which confer root specificity to genes of interest operably linked to them.

Sequence 1354 BP; 321 A; 353 C; 325 G; 355 T; 0 other;

Query Match 76.9%; Score 1354; DB 21; Length 1354;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 1354; Conservative 0; Indels 0; Gaps 0;



QY 1 ctcgagatcttctgatatgaagaaggaattgtagcgaacccgaggtcttccaaggcacgccaag 60  
 Db 1 ctcgagatcttctgatatgaagaaggaattgtagcgaacccgaggtcttccaaggcacgccaag 60  
 QY 61 cgcatactgcgcagctgaggtgctgcgtctgatactgcgaaagagactctgattgttcgtcat 120  
 Db 61 cgcatactgcgcagctgaggtgctgcgtctgatactgcgaaagagactctgattgttcgtcat 120  
 QY 121 cgcgagcttcagatcttggtctccatgaccccaagattgtttgcgcgcgcgctgtaatgagc 180  
 Db 121 cgcgagcttcagatcttggtctccatgaccccaagattgtttgcgcgcgcgctgtaatgagc 180  
 QY 181 agacgcgcagacccgcgaacccggtctctccgaataccaattgttagaataagcgcgacaag 240  
 Db 181 agacgcgcagacccgcgaacccggtctctccgaataccaattgttagaataagcgcgacaag 240  
 QY 241 cagcgaaacaatccgagagacatagtttgggggagagcagatagcttgagagaggaag 300  
 Db 241 cagcgaaacaatccgagagacatagtttgggggagagcagatagcttgagagaggaag 300  
 QY 301 aacaaatagtgacagcgtatagattcctctctgctcctctgttaacctcttcaatctaat 360  
 Db 301 aacaaatagtgacagcgtatagattcctctctgctcctctgttaacctcttcaatctaat 360  
 QY 361 aactcctatcaaggttcgagccatcaagcgaaaccagctcgcggtccacgaacttgggatt 420  
 Db 361 aactcctatcaaggttcgagccatcaagcgaaaccagctcgcggtccacgaacttgggatt 420  
 QY 421 gggcttctgagcagcgcgactggtctctctgctcgtcgtgagctctgtctgtgagacgtgt 480  
 Db 421 gggcttctgagcagcgcgactggtctctctgctcgtcgtgagctctgtctgtgagacgtgt 480  
 QY 481 gctcgcgcgtctaaacatctctgtgttttgagacgaacttcggtgacacggttact 540  
 Db 481 gctcgcgcgtctaaacatctctgtgttttgagacgaacttcggtgacacggttact 540  
 QY 541 ggcgtcgcgcgaagaattgacctatacagtgcctgagcgttcgaactgcagagcgttgaatcc 600  
 Db 541 ggcgtcgcgcgaagaattgacctatacagtgcctgagcgttcgaactgcagagcgttgaatcc 600  
 QY 601 gaggtcgccagctagcagagcaaacgcgtgagctgcatgctgtacgagcttataactg 660  
 Db 601 gaggtcgccagctagcagagcaaacgcgtgagctgcatgctgtacgagcttataactg 660  
 QY 661 agctctactgcgtacgttagatagcacaagcgagatccagaaggggggcaagta 720  
 Db 661 agctctactgcgtacgttagatagcacaagcgagatccagaaggggggcaagta 720  
 QY 721 ggcatacgccccctcaattttgtacaccccttatacctaattgattatgataa 780  
 Db 721 ggcatacgccccctcaattttgtacaccccttatacctaattgattatgataa 780  
 QY 781 gtgtagaaaaatacaaaatttagatagatlaaaaaatctgttcttaactcttaacta 840  
 Db 781 gtgtagaaaaatacaaaatttagatagatlaaaaaatctgttcttaactcttaacta 840  
 QY 841 ataagctgttgcataaattagcgaagaagtttagaatgatacctaattttagactata 900  
 Db 841 ataagctgttgcataaattagcgaagaagtttagaatgatacctaattttagactata 900  
 QY 901 ccccttaaatagatlaattatgttagatggtcccaactagctaaanaacagttaacgtta 960  
 Db 901 ccccttaaatagatlaattatgttagatggtcccaactagctaaanaacagttaacgtta 960  
 QY 961 gctctagatgttttagaacaatggtcctaacaacacatataatgagcctactgcggatcct 1020  
 Db 961 gctctagatgttttagaacaatggtcctaacaacacatataatgagcctactgcggatcct 1020  
 QY 1021 ctgggttcagctcagcactacacagcttgacttaactctccgacacacactaaacca 1080  
 Db 1021 ctgggttcagctcagcactacacagcttgacttaactctccgacacacactaaacca 1080

QY 1081 gtctgctcgctgcgccctgtttctccgaccgacccattcccgatgtagcgtacccgacttc 1140  
 Db 1081 gtctgctcgctgcgccctgtttctccgaccgacccattcccgatgtagcgtacccgacttc 1140  
 QY 1141 gccctctcgtagcgcctccgctccctgttctctgttttctcgttgagcgtcgtatccgtgac 1200  
 Db 1141 gccctctcgtagcgcctccgctccctgttctctgttttctcgttgagcgtcgtatccgtgac 1200  
 QY 1201 aaatagatctgcgtctcgcaacgatatgactatccctcgctgctgtagttagc 1260  
 Db 1201 aaatagatctgcgtctcgcaacgatatgactatccctcgctgctgtagttagc 1260  
 QY 1261 aactagaanaattatgctctcatgttggtcttcttttgccctcctaatttctcgtcg 1320  
 Db 1261 aactagaanaattatgctctcatgttggtcttcttttgccctcctaatttctcgtcg 1320  
 QY 1321 tcgcacactctatagctgctgagggagtgcggggtac 1354  
 Db 1321 tcgcacactctatagctgctgagggagtgcggggtac 1354

## RESULT 7

AAZ52235 standard; DNA; 1348 BP.

AAZ52235;

18-JUL-2000 (first entry)

Maize glycine-rich protein 3 gene 5' regulatory element #2.

Maize; glycine-rich protein 3; GRP3; 5' regulatory element;

root specific gene expression; root abundant gene; monootyledon;

pathogen resistance; pest; herbicide; growth rate; ds.

Zea mays.

Location/Qualifiers

Key TATA-box

23-MAR-2000.

10-SEP-1999; 99WO-EP06692.

11-SEP-1998; 98EP-0117251.

(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.

Feix G, Wulff D;

WPI: 2000-271382/23.

Nucleic acid sequence is used for cloning and expressing a root

specific or root abundant gene in a plant -

Claim 2; Page 50; 60pp; English.

The present sequence is a 5' regulatory element of maize glycine-rich protein 3 (GRP3) gene. It corresponds to positions 413-1760 of the partial genomic clone zmgp3. The present sequence is useful for cloning and expressing root specific or root abundant genes in plants, especially monocots which provide high expression efficiency and high tissue specificity. Root preferred gene expression provides several advantages to plants e.g. resistance to pathogens, pests, herbicides and adverse weather conditions, modification of growth rate and alteration of root tissue function. This sequence also provides a means of isolating related regulatory sequences of other plant species which confer root specificity to genes of interest operably linked to them.



5Q Sequence 1348 BP: 331 A; 355 C; 296 G; 366 T; 0 other;

Query Match 76.6%; Score 1348; DB 21; Length 1348;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 413 ttggatgtggttttggcgaacccgacgtgtctgtcgtcgtggaatctgtctgtg 472  
DB 1 ttggatgtggttttggcgaacccgacgtgtctgtcgtcgtggaatctgtctgtg 60  
OY 473 gagctgtgtctcgcgtcctaacaatctctgtgttttggcgaacattcgcgtggccacg 532  
DB 61 gagctgtgtctcgcgtcctaacaatctctgtgttttggcgaacattcgcgtggccacg 120  
OY 533 cgttaacgcgtctgtcgtccaagaattgacctatacatgtcctgtgcgttaagtcgaagc 592  
DB 121 cgttaacgcgtctgtcgtccaagaattgacctatacatgtcctgtgcgttaagtcgaagc 180  
OY 593 ttgaatccgaagtcgcagtaagcaaacgtgagcgtgcatgtcgttaacgcgtttatt 652  
DB 181 ttgaatccgaagtcgcagtaagcaaacgtgagcgtgcatgtcgttaacgcgtttatt 240  
OY 653 aataactagctctactcgtcgttaagcgtatagcaacgaagcgcgtgacgaaggggg 712  
DB 241 aataactagctctactcgtcgttaagcgtatagcaacgaagcgcgtgacgaaggggg 300  
OY 713 gcaagtgaggccatgtgccccctcaattttgtacacccctttataccatgattatt 772  
DB 301 gcaagtgaggccatgtgccccctcaattttgtacacccctttataccatgattatt 360  
OY 773 agtataagtgtagaaaaaatcaaatattttagatagtaglaaaaaatctgttctaactc 832  
DB 361 agtataagtgtagaaaaaatcaaatattttagatagtaglaaaaaatctgttctaactc 420  
OY 833 taaaactaatagctagtgcttaaaaaattagccaagaagtttagaatggaactaatgt 892  
DB 421 taaaactaatagctagtgcttaaaaaattagccaagaagtttagaatggaactaatgt 480  
OY 893 tagctataccctttaaatgaatgaatgaatgttagatggccaaactagtaaaacaggt 952  
DB 481 tagctataccctttaaatgaatgaatgaatgttagatggccaaactagtaaaacaggt 540  
OY 953 aacagtgatctctagatgttttagaacaatggtccaaacaacatattatagctactgc 1012  
DB 541 aacagtgatctctagatgttttagaacaatggtccaaacaacatattatagctactgc 600  
OY 1013 cggatccctcgtgtcagtcctcagcatctacagctcgtacttaacttcccgacacac 1072  
DB 601 cggatccctcgtgtcagtcctcagcatctacagctcgtacttaacttcccgacacac 660  
OY 1073 ctaaacccagctcgtcgtcgtccctgttcccgacgaacccatctccgaatgagctgc 1132  
DB 661 ctaaacccagctcgtcgtcgtccctgttcccgacgaacccatctccgaatgagctgc 720  
OY 1133 ccgacttcgcccctcgttagcgcctcgtccctgttctgttttctcgttgacgtcgc 1192  
DB 721 ccgacttcgcccctcgttagcgcctcgtccctgttctgttttctcgttgacgtcgc 780  
OY 1193 cgttcgacaattatgattcgtcgttcgcaagaatataccctcgtcgtcgtg 1252  
DB 781 cgttcgacaattatgattcgtcgttcgcaagaatataccctcgtcgtcgtg 840  
OY 1253 acttgaagaactagaanaattatgtctccatgtgtcttttggcccccctcaaatcttc 1312  
DB 841 acttgaagaactagaanaattatgtctccatgtgtcttttggcccccctcaaatcttc 900  
OY 1313 gtccctggtccgcaactctatagctgcgggaagtgcggggtacagtaatctgaag 1372  
DB 901 gtccctggtccgcaactctatagctgcgggaagtgcggggtacagtaatctgaag 960  
OY 1373 tcgaacaatgtatgcttactatctatgtcccggtcagtaataatcagttgcgaagat 1432

DB 961 tcgaacagtgatgagcgtactatctaattcccggtgcgaatataatcagttgccgacgat 1020  
OY 1433 ggggaatctctagttttggacaagaacaaagcgaactgtatgctagcttaattatccaga 1492  
DB 1021 ggggaatctctagttttggacaagaacaaagcgaactgtatgctagcttaattatccaga 1080  
OY 1493 ggatcgaattcttacaagtgctcgtcgaacaatcgaatggaattggaatggaacgatatat 1552  
DB 1081 ggatcgaattcttacaagtgctcgtcgaacaatcgaatggaattggaatggaacgatatat 1140  
OY 1553 gctaatggtttcttcttatacgaatcgtgtcgaacagtgatcgaatlaacaagtctct 1612  
DB 1141 gctaatggtttcttcttatacgaatcgtgtcgaacagtgatcgaatlaacaagtctct 1200  
OY 1613 cgcctcgtatcgaatctcgaatcgaacatggaacccatctgcaccccaacgcggggcg 1672  
DB 1201 cgcctcgtatcgaatctcgaatcgaacatggaacccatctgcaccccaacgcggggcg 1260  
OY 1673 aaccgaaacatcgcgtccatgcaacgcccccgagctataataatcgaatgca 1732  
DB 1261 aaccgaaacatcgcgtccatgcaacgcccccgagctataataatcgaatgca 1320  
OY 1733 atgcagcgggtcatcatcatcgaactca 1760  
DB 1321 atgcagcgggtcatcatcatcgaactca 1348

RESULT 8

AAZ52236  
ID AAZ52236 standard; DNA; 1096 BP.

AAZ52236;  
XX

18-JUL-2000 (first entry)  
XX

Maize glycine-rich protein 3 gene 5' regulatory element #3.  
XX

Maize; glycine-rich protein 3; GRP3; 5' regulatory element;  
XX

root specific gene expression; root abundant gene; monocotyledon;  
KW

pathogen resistance; pest; herbicide; growth rate; ds.  
KW

Zea mays.  
OS

Key location/Qualifiers  
FH TATA\_signal 1048..1055  
FT /tag= a  
FT /standard\_name= "TATA-box"

WO200015662-A1.  
PN

23-MAR-2000.  
PD

10-SEP-1999; 99WO-EP06692.  
PF

11-SEP-1998; 98EP-0117251.  
PR

(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.  
PA

Felix G, Wulff D;  
PI

WP1; 2000-271382/23.  
DR

Nucleic acid sequence is used for cloning and expressing a root  
PT specific or root abundant gene in a plant -

Claim 3; Page 50-51; 60pp; English.  
PS

The present sequence is a 5' regulatory element of maize glycine-rich  
CC protein 3 (GRP3) gene. It corresponds to positions 665-1760 of the  
CC partial genomic clone zmGRP3. The present sequence is useful for cloning  
CC and expressing root specific or root abundant genes in plants,  
CC especially monocots which provide high expression efficiency and high  
CC tissue specificity. Root preferred gene expression provides several

CC advantages to plants e.g. resistance to pathogens, pests, herbicides and  
 CC adverse weather conditions, modification of growth rate and alteration of  
 CC root tissue function. This sequence also provides a means of isolating  
 CC related regulatory sequences of other plant species which confer root  
 CC specificity to genes of interest operably linked to them.

XX Sequence 1096 BP; 288 A; 293 C; 221 G; 294 T; 0 other;

Query Match 62.3%; Score 1096; DB 21; Length 1096;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-311;  
 Matches 1096; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 665 ctactcgctacgttagctatagcaccagaagcgagatccagaaggggggaagtagagcc 724
    |||||||
Db 1 ctactcgctacgttagctatagcaccagaagcgagatccagaaggggggaagtagagcc 60

Qy 725 atggcccccccaatttgttacacccttatacctaataatgataatgataatgataatg 784
    |||||||
Db 61 atggcccccccaatttgttacacccttatacctaataatgataatgataatgataatg 120

Qy 785 agaaaaatacaaatcttagatagataaaaaatctgttcaaatctctaataactatag 844
    |||||||
Db 121 agaaaaatacaaatcttagatagataaaaaatctgttcaaatctctaataactatag 180

Qy 845 ctactgctaaatctagccaaaggttagaatgatacaataatgtttagctataacct 904
    |||||||
Db 181 ctactgctaaatctagccaaaggttagaatgatacaataatgtttagctataacct 240

Qy 905 ttaataatgataatctgttagatgagcccaactagctaaacagttacagtagctc 964
    |||||||
Db 241 ttaataatgataatctgttagatgagcccaactagctaaacagttacagtagctc 300

Qy 965 tagatgtttaaaatagggccaaacacatattatagacctctacgctcgagatctctcg 1024
    |||||||
Db 301 tagatgtttaaaatagggccaaacacatattatagacctctacgctcgagatctctcg 360

Qy 1025 gtctacgtctagcactacacagctgactcaatcttccgcacacacacttaaacagctc 1084
    |||||||
Db 361 gtctacgtctagcactacacagctgactcaatcttccgcacacacacttaaacagctc 420

Qy 1085 gctcgtcgccctgttctccgcacacacacacacacacacacacacacacacacacac 1144
    |||||||
Db 421 gctcgtcgccctgttctccgcacacacacacacacacacacacacacacacacacac 480

Qy 1145 ctctgtagcgctcgcctcctgtcctgttcttctcgtgacgtcgatcgctcgacaat 1204
    |||||||
Db 481 ctctgtagcgctcgcctcctgtcctgttcttctcgtgacgtcgatcgctcgacaat 540

Qy 1205 tagatctcgtcgtcgcacagatatgactatccccctgagcgtcgtagttagcgaact 1264
    |||||||
Db 541 tagatctcgtcgtcgcacagatatgactatccccctgagcgtcgtagttagcgaact 600

Qy 1265 agaaaataatgctctatagtggtcttcttggccccctcctaatttctgctcgtgctcg 1324
    |||||||
Db 601 agaaaataatgctctatagtggtcttcttggccccctcctaatttctgctcgtgctcg 660

Qy 1325 ccaactctatactcgagagtgccggggtgacgctatcgtaactctgaagtcgaacgctgat 1384
    |||||||
Db 661 ccaactctatactcgagagtgccggggtgacgctatcgtaactctgaagtcgaacgctgat 720

Qy 1385 ggcgtactactataatgtcccggtgcagtaataatcactgttgcgcgaagatggaatcttag 1444
    |||||||
Db 721 ggcgtactactataatgtcccggtgcagtaataatcactgttgcgcgaagatggaatcttag 780

Qy 1445 ttcttgacagaacaacaggaactgctatgctagctaatatccagagagatcgatttc 1504
    |||||||
Db 781 ttcttgacagaacaacaggaactgctatgctagctaatatccagagagatcgatttc 840

Qy 1505 taacgtgtagctgcaacaacatcgatgcaatgtgcatcagacagatatatgcaaatggtttt 1564
    |||||||
Db 841 taacgtgtagctgcaacaacatcgatgcaatgtgcatcagacagatatatgcaaatggtttt 900
  
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```

Qy 1565 ctctatcgatactgctgttcaacagtgctacatccagattacagagttctctcgccctgacgg 1624
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Db 901 ctctatcgatactgctgttcaacagtgctacatccagattacagagttctctcgccctgacgg 960

Qy 1625 atctcatgacacatggaacacacacatctgtcacaacccaacgagggggggaacccaacaaat 1684
    |||||||
Db 961 atctcatgacacatggaacacacacatctgtcacaacccaacgagggggggaacccaacaaat 1020

Qy 1685 cgcgtccatgacagaccccccgagctatataatccatgcaatgcatgcaagcggttc 1744
    |||||||
Db 1021 cgcgtccatgacagaccccccgagctatataatccatgcaatgcatgcaagcggttc 1080

Qy 1745 atcatcatcgactcca 1760
    |||||||
Db 1081 atcatcatcgactcca 1096
  
```

RESULT 9  
 AA52237 standard; DNA; 746 BP.

AA52237;

18-JUL-2000 (first entry)

Maize glycine-rich protein 3 gene 5' regulatory element #4.

Maize: glycine-rich protein 3; GRP3; 5' regulatory element;

KW root specific gene expression; root abundant gene; monococtyledon;

KW pathogen resistance; pest; herbicide; growth rate; ds.

OS Zea mays.

XX Key Location/Qualifiers

FT TATA\_signal 698..705

FT /\*\*tag= a

FT /standard\_name= "TATA-box"

PN W0200015662-A1.

PN 23-MAR-2000.

PD 10-SEP-1999; 99WO-EP06692.

PE 11-SEP-1998; 98EP-0117251.

PR (AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.

PA Feix G. Wulff D;

PI WPI: 2000-271382/23.

DR Nucleic acid sequence is used for cloning and expressing a root

XX specific or root abundant gene in a plant -

PT Claim 3; Page 51; 60pp; English.

PS The present sequence is a 5' regulatory element of maize glycine-rich

XX protein 3 (GRP3) gene. It corresponds to positions 1015-1760 of the

CC partial genomic clone zmGRP3. The present sequence is useful for cloning

CC and expressing root specific or root abundant genes in plants,

CC especially monococts which provide high expression efficiency and high

CC tissue specificity. Root preferred gene expression provides several

CC advantages to plants e.g. resistance to pathogens, pests, herbicides and

CC adverse weather conditions, modification of growth rate and alteration of

CC root tissue function. This sequence also provides a means of isolating

CC related regulatory sequences of other plant species which confer root

CC specificity to genes of interest operably linked to them.

XX Sequence 746 BP; 169 A; 225 C; 160 G; 192 T; 0 other;

Query Match 42.4%; Score 746; DB 21; Length 746;

Best Local Similarity 100.0%; Pred. No. 2,6e-208; Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1015	gactcttcggttcagctctctagcatctaacgactgactcttaattctccgacacact	1074						
Db	1	gactcttcggttcagctctctagcatctaacgactgactcttaattctccgacacact	60						
QY	1075	aaacagctctgctcgtccctcgtcttcgcccacacacacacacacacacacacac	1134						
Db	61	aaacagctctgctcgtccctcgtcttcgcccacacacacacacacacacacacac	120						
QY	1135	gaactcgcccttcgtagcgccctcgcccttcgtcttcttcgttcgtagcgatccg	1194						
Db	121	gaactcgcccttcgtagcgccctcgcccttcgtcttcttcgttcgtagcgatccg	180						
QY	1195	ctcgacaattagatctgctcgtcgcgaagatagactataccctcgctcgatgac	1254						
Db	181	ctcgacaattagatctgctcgtcgcgaagatagactataccctcgctcgatgac	240						
QY	1255	ttgacgaactagaataatgatgctcctcatgtgtctttttggccctcctaatttcgt	1314						
Db	241	ttgacgaactagaataatgatgctcctcatgtgtctttttggccctcctaatttcgt	300						
QY	1315	ccctgcctccgcaactctatagctcgcggagtgcgggatccgtatcgatgaatcgaatc	1374						
Db	301	ccctgcctccgcaactctatagctcgcggagtgcgggatccgtatcgatgaatcgaatc	360						
QY	1375	gaacagtgatgctgctactatctaatgtccgtgcgagtaatactactgttcgcgaatgag	1434						
Db	361	gaacagtgatgctgctactatctaatgtccgtgcgagtaatactactgttcgcgaatgag	420						
QY	1435	gaactctagttttgacagaaaccaaaggcaactgctatgctagctaatattccagaga	1494						
Db	421	gaactctagttttgacagaaaccaaaggcaactgctatgctagctaatattccagaga	480						
QY	1495	gactgattttctaacagctgctatgctcgaacaatcgatgcaattggcaatcgaagataatg	1554						
Db	481	gactgattttctaacagctgctatgctcgaacaatcgatgcaattggcaatcgaagataatg	540						
QY	1555	taatggtttcttctatcgatagctggttcaacagtgcaatcagatctagaagttcttcg	1614						
Db	541	taatggtttcttctatcgatagctggttcaacagtgcaatcagatctagaagttcttcg	600						
QY	1615	ccctgactcgatctcatcgcacatgacacccatctgcacacccacgagcgaggagaa	1674						
Db	601	ccctgactcgatctcatcgcacatgacacccatctgcacacccacgagcgaggagaa	660						
QY	1675	ccggaacatcgcttcacatgacgacaccccgacgactataataacatgcaatgcaat	1734						
Db	661	ccggaacatcgcttcacatgacgacaccccgacgactataataacatgcaatgcaat	720						
QY	1735	gcacgaggtcatcatcatcgactcca	1760						
Db	721	gcacgaggtcatcatcatcgactcca	746						
RESULT 10									
AAZ52238									
ID	AAZ52238 standard; DNA: 554 BP.								
XX									
AC	AAZ52238:								
XX									
DT	18-JUL-2000 (first entry)								
XX									
DE	Maize glycine-rich protein 3 gene 5' regulatory element #5.								
XX									
KM	Maize; glycine-rich protein 3; GRP3; 5' regulatory element;								
KM	root specific gene expression; root abundant gene; monocotyledon;								
KM	pathogen resistance; pest; herbicide; growth rate; ds.								
XX									
OS	Zea mays.								
XX									
FH	Key Location/Qualifiers								

FT	TATA_signal	506..513	
FT		/tag=	a
FT		/standard_name=	"TATA box"
PN	WO200015662-A1.		
XX			
PD	23-MAR-2000.		
XX			
PF	10-SEP-1999;	99WO-EP06692.	
XX			
PR	11-SEP-1998;	98EP-0117251.	
PA	(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.		
PI	Feix G, Wulff D:		
XX			
DR	WPI, 2000-271382/23.		
XX			
PT	Nucleic acid sequence is used for cloning and expressing a root		
PT	specific or root abundant gene in a plant	-	
XX			
PS	Claim 3; Page 51; 60pp; English.		
XX			
CC	The present sequence is a 5' regulatory element of maize glycine-rich		
CC	protein 3 (GRP3) gene. It corresponds to positions 1207-1760 of the		
CC	partial genomic clone zmGRP3. The present sequence is useful for cloning		
CC	and expressing root specific or root abundant genes in plants,		
CC	especially monocots which provide high expression efficiency and high		
CC	tissue specificity. Root preferred gene expression provides several		
CC	advantages to plants e.g. resistance to pathogens, pests, herbicides and		
CC	adverse weather conditions, modification of growth rate and alteration of		
CC	root tissue function. This sequence also provides a means of isolating		
CC	related regulatory sequences of other plant species which confer root		
CC	specificity to genes of interest operably linked to them.		
XX			
SQ	Sequence 554 BP; 138 A; 149 C; 127 G; 140 T; 0 other;		
Query Match			
Best Local Similarity 31.5%; Score 554; DB 21; Length 554;			
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1207	gactcgcctcgtcgcgaacgatactatccctcgctcggtgagcttgacgaactag	1266
Db	1	gactcgcctcgtcgcgaacgatactatccctcgctcggtgagcttgacgaactag	60
QY	1267	aaaattatgctctcaatggtctcttttggccctcctaatttctgctcgtcgcgc	1326
Db	61	aaaattatgctctcaatggtctcttttggccctcctaatttctgctcgtcgcgc	120
QY	1327	actctatagctcgaggatgctgggttaccgtatcgtgaatctgaatcgaacagtatgg	1386
Db	121	actctatagctcgaggatgctgggttaccgtatcgtgaatctgaatcgaacagtatgg	180
QY	1387	cgtaactatcattgctcccggtcgaatcaatacactgttcgacgagctgggaatcttagt	1446
Db	181	cgtaactatcattgctcccggtcgaatcaatacactgttcgacgagctgggaatcttagt	240
QY	1447	ttgacagaaccaaaggcaactgctatgctagctaatattccacagagatcgaattcta	1506
Db	241	ttgacagaaccaaaggcaactgctatgctagctaatattccacagagatcgaattcta	300
QY	1507	cagtgcctagctgcaacatcgaatggaattggcatcagaacgatatgctaatggtttct	1566
Db	301	cagtgcctagctgcaacatcgaatggaattggcatcagaacgatatgctaatggtttct	360
QY	1567	ttatcgaatcgttgcacaagtgcgatccagattacaagaattctcgcctgtagat	1626
Db	361	ttatcgaatcgttgcacaagtgcgatccagattacaagaattctcgcctgtagat	420
QY	1627	ctcatcgacatggaacccaatctgcacaaccaaagcgaggcgaggaaacccaacatcg	1686
Db	421	ctcatcgacatggaacccaatctgcacaaccaaagcgaggcgaggaaacccaacatcg	480

Oy 1687 cgtccatgcagacccccacgcagctataatcccatgcatgcaatgcagcgggtcat 1746  
 |||||||  
 Db 481 cgtccatgcagacccccacgcagctataatcccatgcaatgcagcgggtcat 540  
 |||||||  
 Oy 1747 catcatcagactcca 1760  
 |||||||  
 Db 541 catcatcagactcca 554

## RESULT 11

AAZ52239  
 ID AAZ52239 standard; DNA; 406 BP.  
 XX  
 AC AAZ52239;

18-JUL-2000 (first entry)

Maize glycine-rich protein 3 gene 5' regulatory element #6.

Maize; glycine-rich protein 3; GRP3; 5' regulatory element;  
 root specific gene expression; root abundant gene; monocotyledon;  
 pathogen resistance; pest; herbicide; growth rate; ds.

Zea mays.

Key Location/Qualifiers  
 FT TATA\_signal 358..365  
 FT /\*tag= a  
 FT /standard\_name= "TATA box"

W0200015662-A1.

23-MAR-2000.

10-SEP-1999; 99WO-EP06692.

11-SEP-1998; 98EP-0117251.

(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.

Feix G, Wulff D;

WPI: 2000-271382/23.

Nucleic acid sequence is used for cloning and expressing a root  
 specific or root abundant gene in a plant -

Claim 3; Page 52; 60pp; English.

The present sequence is a 5' regulatory element of maize glycine-rich  
 protein 3 (GRP3) gene. It corresponds to positions 1355-1760 of the  
 partial genomic clone zmgRP3. The present sequence is useful for cloning  
 CC and expressing root specific or root abundant genes in plants,  
 CC especially monocots which provide high expression efficiency and high  
 CC tissue specificity. Root preferred gene expression provides several  
 CC advantages to plants e.g. resistance to pathogens, pests, herbicides and  
 CC adverse weather conditions, modification of growth rate and alteration of  
 CC root tissue function. This sequence also provides a means of isolating  
 CC related regulatory sequences of other plant species which confer root  
 CC specificity to genes of interest operably linked to them.

Sequence 406 BP; 112 A; 108 C; 89 G; 97 T; 0 other;

Query Match 23.1%; Score 406; DB 21; Length 406;

Best Local Similarity 100.0%; Pred. No. 1e-106; Indels 0; Gaps 0;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1355 cgtatcgtgatactgaatgcgaacagtgatgctgactatcctaattcccgctgcaat 1414  
 |||||||  
 Db 1 cgtatcgtgatactgaatgcgaacagtgatgctgactatcctaattcccgctgcaat 60

Oy 1415 atcactgtccgcagacgatggaaatcctctagtttttgacagaaaccaaagcaactgcatgc 1474  
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 Db 61 atcactgtccgcagacgatggaaatcctctagtttttgacagaaaccaaagcaactgcatgc 120  
 |||||||  
 Oy 1475 tagctaattaatccagagagatcgattctctacagtgctagctgcgaacaatcgatgcaat 1534  
 |||||||  
 Db 121 tagctaattaatccagagagatcgattctctacagtgctagctgcgaacaatcgatgcaat 180  
 |||||||  
 Oy 1535 tggcatcaagacatatgtctgttttcttcttacagatcgtgtgccaagtgcgcatc 1594  
 |||||||  
 Db 181 tggcatcaagacatatgtctgttttcttcttacagatcgtgtgccaagtgcgcatc 240  
 |||||||  
 Oy 1595 cagattcacagatctctctgccttgatcggatctcatcgcacatggacacctgcgca 1654  
 |||||||  
 Db 241 cagattcacagatctctctgccttgatcggatctcatcgcacatggacacctgcgca 300  
 |||||||  
 Oy 1655 acccaacgcgggcggggaacccgaaacatcgcgttcacatgcagacccacagcatat 1714  
 |||||||  
 Db 301 acccaacgcgggcggggaacccgaaacatcgcgttcacatgcagacccacagcatat 360  
 |||||||  
 Oy 1715 aaataccatgcaatgcaatgcagcggtcatcatcatcagactcca 1760  
 |||||||  
 Db 361 aaataccatgcaatgcaatgcagcggtcatcatcatcagactcca 406  
 |||||||

## RESULT 12

AAZ52240  
 ID AAZ52240 standard; DNA; 190 BP.  
 XX  
 AC AAZ52240;

18-JUL-2000 (first entry)

Maize glycine-rich protein 3 gene 5' regulatory element #7.

Maize; glycine-rich protein 3; GRP3; 5' regulatory element;  
 root specific gene expression; root abundant gene; monocotyledon;  
 pathogen resistance; pest; herbicide; growth rate; ds.

Zea mays.

Key Location/Qualifiers  
 FT TATA\_signal 142..149  
 FT /\*tag= a  
 FT /standard\_name= "TATA box"

W0200015662-A1.

23-MAR-2000.

10-SEP-1999; 99WO-EP06692.

11-SEP-1998; 98EP-0117251.

(AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.

Feix G, Wulff D;

WPI: 2000-271382/23.

Nucleic acid sequence is used for cloning and expressing a root  
 specific or root abundant gene in a plant -

Claim 3; Page 52; 60pp; English.

The present sequence is a 5' regulatory element of maize glycine-rich  
 protein 3 (GRP3) gene. It corresponds to positions 1571-1760 of the  
 partial genomic clone zmgRP3. The present sequence is useful for cloning  
 CC and expressing root specific or root abundant genes in plants,  
 CC especially monocots which provide high expression efficiency and high  
 CC tissue specificity. Root preferred gene expression provides several  
 CC advantages to plants e.g. resistance to pathogens, pests, herbicides and  
 CC adverse weather conditions, modification of growth rate and alteration of

CC root tissue function. This sequence also provides a means of isolating  
CC related regulatory sequences of other plant species which confer root  
CC specificity to genes of interest operably linked to them.  
XX  
SQ Sequence 190 BP; 50 A; 65 C; 42 G; 33 T; 0 other;

Query Match 10.8%; Score 190; DB 21; Length 190;  
Best Local Similarity 100.0%; Pred. No. 1,5e-45;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1571 cgatcgtggtcaacagtcggtccagattacagagttctctgcgcctgcatcgatctca 1630  
|||  
Db 1 cgatcgtggtcaacagtcggtccagattacagagttctctgcgcctgcatcgatctca 60  
OY 1631 tcgcacatggagaccacatctgccaacccaacgcgggcgggagaccggaacatcgctc 1690  
|||  
Db 61 tcgcacatggagaccacatctgccaacccaacgcgggcgggagaccggaacatcgctc 120  
OY 1691 catgacgacccccacgacgtatataatccatgcatgcatgacgaggtcatc 1750  
|||  
Db 121 catgacgacccccacgacgtatataatccatgcatgcatgacgaggtcatc 180  
OY 1751 atcgactcca 1760  
|||  
Db 181 atcgactcca 190

## RESULT 13

AAS46518/c  
ID AAS46518 standard; DNA; 5026 BP.

XX AAS46518;

DT 18-DEC-2001 (first entry)

XX Tumour suppressor gene derived chemically modified sequence #240.

XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic;  
KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;

KW cytosine methylation; ds.

XX Homo sapiens.

XX MO200168912-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-EP02955.

XX 15-MAR-2000; 2000DE-1013847.

XX 06-APR-2000; 2000DE-1019058.

XX 07-APR-2000; 2000DE-1019173.

XX 30-JUN-2000; 2000DE-1032529.

XX 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI: 2001-602752/68.

XX Fragments of chemically modified genes associated with tumour suppressor  
XX genes and oncogenes, useful in designing primers and probes for  
XX analysing diseases associated with cytosine methylation state e.g.  
XX cancer

XX Claim 1; SEQ ID No 240; 27bp; English.

CC The invention relates to a nucleic acid comprising a sequence of 18  
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with  
CC bisulphite, of genes associated with tumour suppression and  
CC oncogenes having a sequence taken from 536 (actually 533 since

CC numbers 408, 458 and 500 are missing from the sequence listing) sequences  
CC (SS) and sequences complementary to (SS). The nucleic acid may be a  
CC peptide nucleic acid-oligonucleotide (PNA) of at least 9 nucleotides and may  
CC form part of a set of probes for detecting the cytosine methylation state  
CC and/or single nucleotide polymorphisms and also to be used in an  
CC array for analysing diseases associated with CpG dinucleotides e.g.  
CC cancers and tumours. The probes can also be used in a method for  
CC ascertaining genetic and/or epigenetic parameters for the diagnosis  
CC and/or therapy of existing diseases or the predisposition to specific  
CC diseases, by analysing cytosine methylations. The parameters may be  
CC compared to another set of genetic and/or epigenetic parameters, the  
CC differences serving as basis for diagnosis and/or prognosis events which  
CC are disadvantages to patients. The present sequence is one of the  
CC 533 genomic sequences derived from tumour suppressor genes and  
CC oncogenes. Sequences with even numbered Seq ID numbers are the  
CC complementary sequence of the corresponding odd numbered sequence (e.g.  
CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence  
CC is missing).  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 5026 BP; 1467 A; 121 C; 1122 G; 2316 T; 0 other;

Query Match 2.8%; Score 48.8; DB 22; Length 5026;  
Best Local Similarity 47.8%; Pred. No. 0.0024;  
Matches 172; Conservative 0; Mismatches 187; Indels 1; Gaps 1;

OY 647 ttattaaactgagctactactgctacgttagctagtcagccacgagcgatccaga 706  
|||  
Db 2597 TTTCTTTAATAATTACCTTAATCTCATTTAATACATACAAAACATCTAATACCA 2538  
OY 707 ggggggggcaagtaggcacatggcccccccaatttggcaccccttatacctaaga 766  
|||  
Db 2537 ATTTCCAAAATAATTAACTCTCACCAACAAATATATAAATAATACATACATATCC 2478  
OY 767 ttattagatgaagtgtgaaaaaataaatttagatagatataaaat-ctgttct 825  
|||  
Db 2477 TTATCAATACCTTAATATTAATAAATCCTTTTAATTAACCATCTTAATATATTTTAAT 2418  
OY 826 aaactcctaaactaagctagctgctaaattgacccaagaagtttagaagatgaac 885  
|||  
Db 2417 ATCTCATTAATTTCAATATACATATATTAATAAATCTTTTCATATTAACCATTAATA 2358  
OY 886 taattgttagctatacccttaataagatattgttagatggcccaactagctaaa 945  
|||  
Db 2357 CGATCTTAATAATTACCCCTTCAAAAACCATATCATATATTAATTAATACATAA 2298  
OY 946 accagttacagttgctctagatgttttagaacaatggcctaacaacatattatagacc 1005  
|||  
Db 2297 ACTAATATACACACATTAATATATTAATTAACCATTAACCAACATCACTAAACCTAAC 2238

## RESULT 14

ABL33775/c  
ID ABL33775 standard; DNA; 7503 BP.

XX ABL33775;

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 1748.

XX Human; immune system disease; cytosine methylation; antiasthmatic;  
KW antiarteriosclerotic; antianaemic; cytosatic; noctropic;

KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KW antirheumatic; antiarthritic; antidiabetic; antiporiatic;

KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
KW gene; ds.

XX Homo sapiens.  
OS  
XX  
XX WO200200928-A2.  
PN  
XX  
XX  
PD 03-JAN-2002.  
XX  
XX  
PF 02-JUL-2001; 2001WO-EP07537.  
XX  
XX  
PR 30-JUN-2000; 2000DE-1032529.  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
XX  
PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
DR WPI; 2002-130909/17.  
XX  
XX  
PT Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation -  
PS  
PS Claim 1; SEQ ID NO 1748; 32pp + Sequence Listing; German.  
XX  
XX The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
CC diseases. The present sequence is a gene of the invention.  
XX  
SQ Sequence 7503 BP; 2091 A; 174 C; 1582 G; 3656 T; 0 other;

Query Match 2.8%; Score 48.4; DB 24; Length 7503;  
Best Local Similarity 49.2%; Pred. No. 0.004;  
Matches 127; Conservative 0; Mismatches 131; Indels 0; Gaps 0;  
QY 745 tacaccccttatacctaagatattagtagtaagtgtagaataaataaatttag 804  
DB 6349 TAAACATTTAAATTAACCTACTATCTTTAAAAAATAACAAAAAATTCAT 6290  
QY 805 atgataaataaacttcttaaatcttaaactaactaagtagctgtaaatagcca 864  
DB 6289 TTACAAATTAATTTTAAAAAACTACTCTAACCAATTAATATATATAAATAACA 6230  
QY 865 aaaggttagaagatgataactaattgttagctatacccttaataagtaattggt 924  
DB 6229 AAAACACTATTCTTAATCTACTATACATTAATTAACCAAAATTAACAAATCA 6170  
QY 925 agatgagcccaactagctaaacagcttaacagctagctagctgttagaacaatgccc 984  
DB 6169 AATTCATCACAAACACCAAAATTTTATATCTACGCAAAATATTTTAAAAAC 6110  
QY 985 taacaacacatattatga 1002  
DB 6109 TAAAAAAACCAATTATTA 6092

RESULT 15  
ABL33796/C  
ID ABL33796 standard; DNA: 5416 BP.  
XX  
XX ABL33796;  
AC  
XX  
XX 26-MAR-2002 (first entry)  
DT  
XX  
XX Human immune system associated gene SEQ ID NO: 1769.  
DE  
XX  
XX Human; immune system disease; cytosine methylation; antiasthmatic;  
KW antiarteriosclerotic; antianaemic; cyostatic; nootropic;

KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KW antihemmatic; antiarthritis; antidiabetic; antipsoriatic;  
KW antinflamatory; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
KW gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200200928-A2.  
PN  
XX  
XX  
PD 03-JAN-2002.  
XX  
XX  
PF 02-JUL-2001; 2001WO-EP07537.  
XX  
XX  
PR 30-JUN-2000; 2000DE-1032529.  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
XX  
PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
DR WPI; 2002-130909/17.  
XX  
XX  
PT Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation -  
PS  
PS Claim 1; SEQ ID NO 1769; 32pp + Sequence Listing; German.  
XX  
XX The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
CC diseases. The present sequence is a gene of the invention.  
XX  
SQ Sequence 5416 BP; 1476 A; 96 C; 1134 G; 2710 T; 0 other;

Query Match 2.7%; Score 47.2; DB 24; Length 5416;  
Best Local Similarity 50.3%; Pred. No. 0.0074;  
Matches 144; Conservative 0; Mismatches 138; Indels 4; Gaps 1;  
QY 715 aaagtaggccatgccccccctcaatttgytaaccccttatccctaagtatttag 774  
DB 3899 AAATACGCCCAATCACATCAATATATTTCTTTAATTCATGTAATCCAAA 3840  
QY 775 tattagtgtagaaaatacaaatltagatagataaataactggtcctaactccta 834  
DB 3839 TATTAATTTACCAACGTATAAATATCCCATATATTAATATATATATATATTC 3780  
QY 835 aaactaagtagctgctaaataagccaaaaggttagaagatgaactaactgttta 894  
DB 3779 AATA----ATCTATTCTCTTAATCATTAATTAATATATCTAATATACAAATATCTTA 3724  
QY 895 gctatacccttaataagatattatgttagatagagcccaaccctagccaacacgtaaa 954  
DB 3723 TTACTAAATTTATATATTTCTAATTTATTTTAAAACTTTATAAAAAACTACTTA 3664  
QY 955 cagttagcttagatgtttagaacaatgagcccaacacacacattat 1000  
DB 3663 TATAAACCACATTTTATATCTCTTAATATTAATTAATTAATTAATTAAT 3618

Search completed: July 30, 2002, 18:07:15  
Job time: 4385 sec







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2002, 16:50:25 ; Search time 56.36 Seconds  
(without alignments)  
7670.599 Million cell updates/sec

Title: US-09-786-835-1  
Perfect score: 1760  
Sequence: 1 ctcgagatgttgatagaag.....ggtcacatcactcactcca 1760

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCBUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	62.2	3.5	7218	1 US-08-232-463-14	Sequence 14, Appl
2	41.4	2.4	1183	2 US-08-731-722-8	Sequence 8, Appl
3	39.6	2.2	1183	2 US-08-731-722-8	Sequence 8, Appl
4	39.6	2.2	2110	4 US-09-419-459-1	Sequence 1, Appl
5	37.4	2.1	7218	1 US-08-232-463-14	Sequence 14, Appl
6	37.2	2.1	625	4 US-08-988-416-919	Sequence 19, App
7	37.2	2.1	713	4 US-08-998-416-956	Sequence 956, App
8	36.8	2.1	8920	2 US-08-446-855A-1	Sequence 1, Appl
9	36.8	2.1	8920	4 US-09-150-741-1	Sequence 32, Appl
10	36	2.0	660	1 US-07-991-867B-32	Sequence 32, Appl
11	36	2.0	660	1 US-08-107-755A-32	Sequence 32, Appl
12	36	2.0	660	2 US-08-544-332-32	Sequence 32, Appl
13	36	2.0	1511	1 US-07-991-867B-8	Sequence 8, Appl
14	36	2.0	1511	1 US-08-107-755A-8	Sequence 8, Appl
15	36	2.0	1511	2 US-08-544-332-8	Sequence 11, Appl
16	36	2.0	4810	3 US-08-852-629-11	Sequence 11, Appl
17	36	2.0	4810	3 US-08-852-629-15	Sequence 15, Appl
18	36	2.0	80246	4 US-09-078-294-4	Sequence 4, Appl
19	35.8	2.0	777	4 US-09-007-119-12	Sequence 12, Appl
20	35.8	2.0	8700	2 US-08-392-625-16	Sequence 16, Appl
21	35.8	2.0	8700	2 US-08-466-961A-16	Sequence 16, Appl
22	35.8	2.0	8700	2 US-08-645-193B-18	Sequence 18, Appl
23	35.8	2.0	10564	1 US-08-206-176-5	Sequence 5, Appl
24	35.6	2.0	2273	3 US-08-714-818-40	Sequence 40, Appl
25	35.6	2.0	2273	4 US-09-265-315-40	Sequence 40, Appl
26	35.6	2.0	2273	4 US-09-265-315-40	Sequence 40, Appl
27	35.6	2.0	2273	4 US-09-266-417-40	Sequence 40, Appl

C 28	35.6	2.0	4291	2 US-08-417-210A-81	Sequence 81, Appl
C 29	35.6	2.0	12730	4 US-09-004-838-91	Sequence 91, Appl
C 30	35.4	2.0	1850	3 US-08-617-860B-32	Sequence 32, Appl
C 31	35.4	2.0	4098	2 US-08-605-106-4	Sequence 4, Appl
C 32	35.2	2.0	731	4 US-08-451-405A-2	Sequence 2, Appl
C 33	35.2	2.0	1103	4 US-09-123-400B-20	Sequence 20, Appl
C 34	35.2	2.0	1167	1 US-08-592-658-1	Sequence 1, Appl
C 35	34.8	2.0	1395	1 US-07-991-867B-25	Sequence 25, Appl
C 36	34.8	2.0	1395	1 US-08-107-755A-25	Sequence 25, Appl
C 37	34.8	2.0	1395	2 US-08-544-332-25	Sequence 25, Appl
C 38	34.8	2.0	2803	3 US-08-949-588-1	Sequence 1, Appl
C 39	34.8	2.0	6768	1 US-08-107-755A-1	Sequence 1, Appl
C 40	34.8	2.0	8457	1 US-07-991-867B-1	Sequence 1, Appl
C 41	34.8	2.0	8457	2 US-08-544-332-1	Sequence 1, Appl
C 42	34.6	2.0	8700	2 US-08-392-625-16	Sequence 16, Appl
C 43	34.6	2.0	8700	2 US-08-466-961A-16	Sequence 16, Appl
C 44	34.6	2.0	8700	2 US-08-645-193B-18	Sequence 18, Appl
C 45	34.4	2.0	80595	4 US-09-078-294-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEFFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: Linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pC-Fls  
US-08-232-463-14



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OY 756 accataatgattattagattagtagtaaaacaaatttagatagatataaat 817
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Db 840 ACCGTCTAATCAATAGTAAATCCAGACCAATAATTTTGCAGATTGTAATACAT 781
OY 818 ctgtctctaaactctaaacaaatagtagtctgtaaaattagccaaaggcttagaat 877
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 ATTATGTAATTAATTAATTAATCTTTTAAAGATATTAATCTTTTAAATAATTAAT 721
OY 878 gatacaactaattgttagctatacccttaataagattattgttagatggtcccaacc 937
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 720 GAAATTAATCTTAATAAGATATTAATTAATTAATTAATTAATTAATTAATTAAT 661
OY 938 tagctaaacacagtaacagtagcttagatgcttagatgcttagatgcttagatgct 991
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 660 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 607
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RESULT 4
US-09-419-459-1
; Sequence 1, Application US/09419459
; Patent No. 6222028
; GENERAL INFORMATION:
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Tsai, Cheng-Fang
; APPLICANT: Chang, Chia-Chieh
; TITLE OF INVENTION: CELLULOSE ENZYMES
; FILE REFERENCE: 08919/037001
; CURRENT APPLICATION NUMBER: US/09/419,459
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2110
; TYPE: DNA
; ORGANISM: Piromyces rhiziniata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(1749)
US-09-419-459-1
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Query Match 2.28; Score 39.6; DB 4; Length 2110;
Best Local Similarity 51.7%; Pred. No. 0.09;
Matches 90; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

OY 752 tttaacaaatgattattagattagtagtaaaacaaatttagatagat 811
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Db 1856 tttaattctattatttttaataaaaaattataagaagaataataataat 1915
OY 812 aaaaactgttctaaactctaaactaaatagtagtctgtaaaattagccaaaggct 871
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Db 1916 aataatgaatgaataaatttttaattattattcttcttaacttaagaataaaagaat 1975
OY 872 tagatgtagcaactaattgttagctatacccttaataaagatttaattgtta 925
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1976 ttaactaaatcaagaatttttaagaatggaatagtattttaataatagcta 2029
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RESULT 5
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
```

```
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300, 6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMKU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15
US-08-232-463-14
```

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Query Match 2.1%; Score 37.4; DB 1; Length 7218;
Best Local Similarity 2.4%; Pred. No. 0.74;
Matches 8; Conservative 188; Mismatches 139; Indels 0; Gaps 0;

OY 4 gagatgttgatagaagaatgtcgagcaacgagctctcgaagcgacgcaacgagc 63
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Db 1386 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1327
OY 64 atccgtcgagtgagtgctgctgtagtgcggaagagcttgctgctgctgcgc 123
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Db 1326 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1267
OY 124 gagctcagattggtctcagatgaccccgatgttggcgcgcgctgtaatgagcga 183
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 1266 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1207
OY 184 cgccagaccgagacggtgtctcgaataatgtagcaatgtagcagcgagcaacgag 243
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 1206 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1147
OY 244 cgaacaacgagagacatgttggtgggagagcagatagcttggaagaagaagac 303
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 1146 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1087
OY 304 aatagtgacagcagatctctctgctcctc 338
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Db 1086 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1052
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RESULT 6
US-08-998-416-919
; Sequence 919, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Pihlpsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
```

```

APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264rtis Corporation
STREET: 3054 Cornwalls Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PR/5-30306/A/GCCL976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 919:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1572RP
US-08-998-416-919

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Query Match          2.1%; Score 37.2; DB 4; Length 625;
Best Local Similarity 61.2%; Pred. No. 0.24;
Matches 60; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Db 194 AATATTTTATTTTATTTTCTAATAAATAAATAATTAATTAATAATAATATTC 253

Oy 822 ttctaactccaactaatagctagtcctaaatt 859
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Db 254 ATTAATACTTAAATATTAATTAATTAATATTAATCTT 291

RESULT 7
US-08-998-416-956
; Sequence 956, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPILL
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264rtis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264tn Carolina
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//08/998.416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: Pp/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 956:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1590UP
US-08-998-416-956

```

```

Query Match          2.1%; Score 37.2; DB 4; Length 713;
Best Local Similarity 61.2%; Pred. No. 0.26;
Matches 60; Conservative 0; Mismatches 38; Indels 0; Gaps 0.

QY      762  aatgattctttagatgaatgaigtgagaaaaatcacaattttagatagataaataacttg 821
          || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      194  AAAATTTTATTTATTTTATTTACTTAAATAAAAAAATTAATTAATTAATTAATTAATTAATTC 253

QY      822  ttctaatctctaaactaatagctagtcgcaaat 859
          || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      254  ATTAAATACTTTAATTTAATTTAATTTAATTTAATTTACTT 291

RESULT
      8
US-08-446-855A-1/c
: Sequence 1, Application US/08446855A
: Patent No. 5849573
:
: GENERAL INFORMATION:
:
: APPLICANT: Stewart, Thomas S
:
: APPLICANT: Flores, Maria V
:
: APPLICANT: O'Sullivan, William J
:
: TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
:
: TITLE OF INVENTION: Phosphate synthetase II
:
: NUMBER OF SEQUENCES: 2
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Nixon & Vanderhye PC
:
: STREET: 1100 NO. 5849573th Glebe Road, 8th Floor
:
: CITY: Arlington
:
: STATE: Virginia
:
: COUNTRY: USA
:
: ZIP: 22201-4714
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: OPERATING SYSTEM: PC-DOS/MS-DOS

```

Query Match	2.1%	Score	36.6	DB	4	Length	8920	
Best Local Similarity	48.1%	Pred. No.	1.2					
Matches 104	Conservative	0	Mismatches	112	Indels	0	Gaps	0

Query Match	2.08;	Score 36;	DB 1;	Length 660;
Best Local Similarity	62.0%;	Pred. NO. 0.57;		
Matches 57; Conservative	0;	Mismatches 35;	Indels 0;	Gaps 0;





```

US-08-544-332-8
: Sequence 8, Application US/08544332
: Patent No. 5935777
: GENERAL INFORMATION:
: APPLICANT: Moyer, Richard W.
: APPLICANT: Hall, Richard L.
: APPLICANT: Gruidl, Michael E.
: TITLE OF INVENTION: No. 5935777e1 Entomopoxvirus Expression System
: NUMBER OF SEQUENCES: 77
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Gerard H. Bencen
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/544,332
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/991,867
: FILING DATE: 07-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/107,755
: FILING DATE: 19-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO 92/14818
: FILING DATE: 12-FEB-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/827,685
: FILING DATE: 30-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/657,584
: FILING DATE: 19-FEB-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Bencen, Gerard H.
: REGISTRATION NUMBER: 35,746
: REFERENCE/DOCKET NUMBER: UFI14.C4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 904-375-8100
: TELEFAX: 904-372-5800
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1511 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Amsacta moorei entemopoxvirus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: complement (18..218)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: complement (234..782)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 852..1511
:
US-08-544-332-8

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Qy      782  tgttgaataaatcaaaattttgatgatgtgtaaaatctgttctaactcaaaacaa 841
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1340  TATGAGAAAAATTAATTATTATTAAAAAAATTAAGATATATCTTCATTCATGTTAAAAAAATTA 1399

Qy      842  taagtagtgcctaaatagccaaaaggttta 873
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Db      1400  TATACATTTGATATAAAATTTCCAAAAAAGTATTA 1431

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Search completed: July 30, 2002, 18:03:08
Job time: 4363 sec
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2002, 16:46:19 ; Search time 1679.9 Seconds  
(without alignments)  
14140.509 Million cell updates/sec

Title: US-09-786-835-1  
Perfect score: 1760  
Sequence: 1 ctgcagatgttgatagaag.....gtcaccatcatcactca 1760

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	287	16.3	583	10	BG842425 MEST30-G0
C 2	105.8	6.0	148	12	BH221366 1006100H0
C 3	72.4	4.1	444	9	AI948280 603039G10
C 4	72.4	4.1	515	10	BF727838
C 5	72.4	4.1	627	9	AW147089 707011D10
C 6	69.6	4.0	451	12	BH225777 1006128D0
C 7	61.4	3.5	465	10	BM381538 MEST35-B
C 8	53.8	3.1	997	12	CNS005TE
C 9	53.4	3.0	1190	12	CNS020N7
C 10	52.8	3.0	436	12	AZ916152 PstI_3-C2
C 11	49.4	2.8	1101	12	CNS0039G
C 12	48.8	2.8	275	12	BH229936 1006155C0
C 13	48.8	2.8	282	12	BH229935 1006155C0
C 14	48.4	2.8	815	12	BH597991 BOHFX52TR
C 15	48.4	2.8	1043	12	CNS0145P
C 16	48.2	2.7	770	12	AO740708 HS_5507_A
C 17	48.2	2.7	1101	12	CNS00EVL

C 18	48.2	2.7	1131	12	CNS034FO	AL27373 Tetradon
C 19	47.6	2.7	1092	12	CNS020K7	AL175696 Tetradon
C 20	47.6	2.7	1203	12	CNS015WU	AL106008 Drosophila
C 21	47.4	2.7	839	12	AQ892711	AO892711 HS_4832_A
C 22	47.4	2.7	1225	12	CNS0161D	AL106171 Drosophila
C 23	47.2	2.7	1101	12	CNS0039G	AL063921 Drosophila
C 24	47.2	2.7	303	12	BH215811	BH215811 1006037A1
C 25	47.2	2.7	1101	12	CNS012BM	AL101356 Drosophila
C 26	46.8	2.7	777	12	BH602454	BH602454 BOHES41TF
C 27	46.6	2.6	560	10	B513308	B5133308 BH160011B
C 28	46.6	2.6	1101	12	CNS016L1	AL106896 Drosophila
C 29	46.6	2.6	1200	12	CNS016CO	AL106578 Drosophila
C 30	46.4	2.6	661	12	CNS020V7	AL209800 Tetradon
C 31	46	2.6	625	12	BH571050	BH571050 BOGH052TR
C 32	45.6	2.6	564	9	AI947590	AI947590 603024D11
C 33	45.6	2.6	975	12	BH179465	BH179465 014_P_10-
C 34	45.4	2.6	788	12	CNS00AK8	AL055582 Drosophila
C 35	45.4	2.6	1086	12	CNS00YXK	AL096962 Drosophila
C 36	45.2	2.6	340	12	BH413738	BH413738 1007034C0
C 37	45.2	2.6	616	9	AV672208	AV672208 AV672208
C 38	45.2	2.6	1159	12	CNS015XR	AL106041 Drosophila
C 39	45	2.6	1101	12	CNS0042W	AL055440 Drosophila
C 40	44.8	2.5	512	10	B1451206	B1451206 kx11h09.Y
C 41	44.8	2.5	556	12	BH446808	BH446808 BOGOT82TR
C 42	44.6	2.5	1201	12	CNS0103V	AL098485 Drosophila
C 43	44.6	2.5	1201	12	CNS016EA	AL106636 Drosophila
C 44	44.4	2.5	226	12	CNS0154S	AL104998 Drosophila
C 45	44.4	2.5	573	9	AU004580	AU004580 AU004580

## ALIGNMENTS

RESULT 1  
BG842425/c  
LOCUS MEST30-G03.T3 ISUM4-TN Zea mays cDNA clone MEST30-G03 3', mRNA  
DEFINITION  
ACCESSION BG842425.2 GI:14244354  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays.  
Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
ciade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 583)  
Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.  
Expressed Sequence Tags from B73 Maize Seedlings and Silks  
Unpublished (2001)  
On May 25, 2001 this sequence version replaced gi:14208747.  
Contact: Patrick S. Schnable  
Schnable Laboratory  
Iowa State University  
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA  
Tel: 515-294-0975  
Fax: 515-294-2299  
Email: schnable@iastate.edu

PCR Primers  
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)  
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)  
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).  
Location/Qualifiers  
1..583  
/organism="Zea mays"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="MEST30-G03"  
/clone\_lib="ISUM4-TN"  
/tissue\_type="Seedling and silk"  
/lab\_host="DH10B"  
/note="Vector: pVT73PAC; Site\_1: EcoRI; Site\_2: NotI;  
ds-cDNA molecules were generated as follows. First-strand





Query Match	Similarity	4.1%	Score 72.4%	DB 9	Length 627
Best Local	Similarity	72.4%	Pred. No. 4e-08		
Matches	113	Conservative	0	Mismatches	31
				Indels	12
				Gaps	1
OY	813	aaaatctgttcttaaatccttaaacataagctagctgtctgaataatagccaaaggctt	872		
Db	529	AAGGTCCTGTTCCAAACCTCTMAACTATATGTGGCATTTAAATTAACCTGAAGGTTT	470		
OY	873	agaatgagttca-----actaatgttacttaacaccttaataagtaattat	920		
Db	469	AAAGGAGTACATATATATGAGCCACTATATGTACTCTTCACTCTCAATATGTCATTAGC	410		
OY	921	tgttagatgagcccaactagcttaaacaccagttaca	956		
Db	409	TGTATGCTGTCTCAACACCAGCTAAACCACTAACA	374		
RESULT	6				
LOCUS	BH235777	451 bp	DNA	linear	GSS 08-NOV-2001
DEFINITION	1006128D01.x1 1006 - Rescemu Grid G Zea mays genomic, DNA				
ACCESSION	BH235777				
VERSION	BH235777.1	GI:16824081			
KEYWORDS	GSS.				
SOURCE	Zea mays.				
ORGANISM	Zea mays				
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; PACC clade: Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 451)				
TITLE	Maize genomic sequences found using engineered Rescemu transposon				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 1006128 row: 2 Class: transposon-tagged. Location/Qualifiers 1..451 /organism="Zea mays" /cultivar="mixed background W23/A188/B73" /db_xref="taxon:4577" /clone_lib="1006 - Rescemu Grid G" /tissue_type="leaf" /dev_stage="adult" /lab_host="DH10B" /note="Organ: leaf; Vector: Rescemu (engineered from pBluescript backbone); Site.1: BamHI; Site.2: BglII; Rescemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmdb.laestate.edu' and follow the links for 'Rescemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."				
BASE COUNT	115 a	123 c	121 g	92 t	

Query Match	4.0%	Score	69.6	DB	12	Length	451
Best Local Similarity	68.6%	Pred. No.	1.9e-07				
Matches	96	Conservative	44			Indels	0
						Gaps	0

Oy	11	tggatgaggaagggaattcgagcaaacgcaggctccaaagcgcgaacgcgcatccgac	70
Db	127	TGGATCGAGCCGCGAATGATGAAGCCGCACCTGTGCACCTCCCAGCAGCGTACCTTCCTGA	186
Oy	71	gcagtggagtgtagtcgatgtgcgcgaagaaggactcgattgttgcgcgacgcgaacttc	130
Db	187	GCAGCGAACACGGTGACTACTATCTCGCGAAGAAGAACTCAACTGTCTCATGTGCGGACGTGT	246
Oy	131	agatttgacctcatgaccgc	150
Db	247	AGTTGGGCTCCATGACC	266
<b>RESULT 7</b>			
LOCUS	BM381538	465 bp	mRNA linear EST 16-JAN-2002
DEFINITION	BM381538	MEST536-B09.univ ISUM6 Zea mays cDNA clone MEST536-B09.3,	mRNA sequence.
ACCESSION	BM381538		
VERSION	BM381538.1	GI:18180328	
KEYWORDS	EST.		
SOURCE	Zea mays.		
ORGANISM	Zea mays		
REFERENCE	Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC		
TITLE	clade: Panicoideae; Andropogoneae; Zea.		
JOURNAL	Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.		
COMMENT	Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones unpublished (2001) Contact: Patrick S. Schnable Schnable Laboratory Iowa State University G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA Tel.: 515-294-0975 Fax: 515-294-2299 Email: schnable@iastate.edu		
FEATURES	Individual basecall and confidence value were assigned using the phred software( <a href="http://www.phrap.org/">http://www.phrap.org/</a> ). Overall sequence quality assessment and vector trimming was conducted using the Lucy software (version 1.165, <a href="http://www.tigr.org/software/lucy">http://www.tigr.org/software/lucy</a> ). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers using a Perl program ( <code>est-process.pl</code> ), written by Dr. Hui-Hsien Chou.		
source	PCR Primers FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG) BACKWARD: primer Sp6 (ATT TAG GTG ACA CTA TAG) Seq primer: universal (GTA AAA CGA CGG CCA GT) POLY-A-yes.  Location/Qualifiers 1..465		

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/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST536-B09"
/clone_id="ISU6"
/tissue_type="mixed"
/lab_host="DH10B"
/note="Vector: pSlip7 (4.43 kb); Site.1: EcoRI; Site.2:
NotI. Tissue samples were collected and partially pooled
prior to RNA extraction. First-strand cDNAs were prepared
from 21 individual pools of oligo-dT selected mRNAs by
priming with 21 different NotI oligo-dT tag primers
(5'-AAGTCGAGAAGATTCGCCGCCGCGCCGNNNNNTTTTATTTTATTTT-3').
Distinguishable 'bar code' tags, (N)6, were used for each
separate first-strand cDNA synthesis. Hence, these bar
code tags can be used to identify the mRNA pool from which
a particular cDNA clone was derived. The 'bar code' tags

```













